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June 25, 2002, 16:12:12; Search time 35.41 Seconds (without alignments) 114.506 Million cell updates/sec
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                                                                                                                                                                               1 MSGLGRSRRGGRSRVDQEER.....SPALPGLKLSADQVALVYST
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                  US-09-854-864-15
909
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Match Length
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                            OM protein
                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
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Sequence 41, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 73, Appl Sequence 74, Appl Sequence 6, Appl	HAT BINDS IE SAME AND METHODS OF US	Length 166;
28 77.5 8.5 75 2 US-08-465-380-41 29 77.5 8.5 75 2 US-08-465-380-41 31 77.5 8.5 75 2 US-08-486-397-6 31 77.5 8.5 75 2 US-08-486-399-6 33 77.5 8.5 75 2 US-08-486-399-6 33 77.5 8.5 75 2 US-08-486-399-6 35 77.5 8.5 75 2 US-08-461-965-6 36 77.5 8.5 75 2 US-08-461-965-6 37 77.5 8.5 75 2 US-08-461-965-41 38 77.5 8.5 75 2 US-08-634-641-6 40 77.5 8.5 75 2 US-08-634-641-41 41 77.5 8.5 75 3 US-09-249-471-41 42 77.5 8.5 75 3 US-09-249-471-41 43 77.5 8.5 75 3 US-09-249-471-41 44 77.5 8.5 75 3 US-09-249-471-41 45 77.5 8.5 75 3 US-09-249-471-41 47 77.5 8.5 75 3 US-09-249-451-6 48 77.5 8.5 75 3 US-09-249-451-6 49 77.5 8.5 75 3 US-09-249-451-6	RESULT 1 US-08-80-72A-6 Sequence 6, Application US/08810572A Fatent No. 5963102 GENERAL INFORMATION: APPLICANT Bram, Richard J. APPLICANT Bram, Richard J. APPLICANT Bram, Richard J. APPLICANT WOR BALOW, GOEZ TITLE OF INVENTION: THEROF TITLE OF INVENTION: THEROF TITLE OF INVENTION: THEROF NUMBER OF SECUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEE: David A. Jackson, ESQ; STREET 411 Hackensack Ave, Continental Plaza, 41 STREET; Hackensack CONTRY: USA CONTRY: USA COMPRY: USA COMP	Query Match 100.0%; Score 909; DB 2; Le

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Bram, Richard J.
APPLICANT: Bram, NUCLEIC SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                               61 TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
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                                                                                                         121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
STREET: Floor
STREET: May Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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100.0%; Pred. No. 3.4e-90;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1340-1-007
                                                                                                                                                                                                                                         Sequence 2, Application US/08810572A Patent No. 5969102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE, DOCKET NUMBER: 1340-
TELECOMMINICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 293 amino acids
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Best Local Similarity 100.(
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
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                                                                                                                                                                     61 TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
                                                                                                                                             61 TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
                                 Gaps
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                                                                   1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                               Indels
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Datemin Selease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/09/290,333
FILING DATE: 12-APP-1999
CLASSIFICATION: <unhaper controvers
                                                                                                                                                                                                                                               121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                           121 ORSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 909; DB 4;
100.0%; Pred. No. 1.7e-90;
iive 0; Mismatches 0;
             Pred. No. 1.7e-90;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-290-333-6
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0
Best Local Similarity 100.0
Matches 166; Conservative
                               Conservative
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           Best Local Similarity
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603 TNSCVTHCPDGSYQDTKKNLCRKCSENC----KTCTEFHNCTECRDGLSLQGSRCSVSC 657
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TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 799;
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                                                                               APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND
TITLE OF INVENTION: EMCODING SAID PROTEASES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 TGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAF----CR
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.1%; Score 04.2,
26.0%; Pred. No. 1.3;
ative 10; Mismatches 34;
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Concell, Gary J.
REGISTATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08976838 Patent No. 5981259 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 799 amino acids TYPE: amino acid
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Best Local Similarity 26.0%
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                       GENERAL INFORMATION:
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CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Denver
                 Patent No. 5866351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                    APPLICANT: Bram, Richard J.
APPLICANT: Bram, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVId A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
, descensions of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE : 201-487-5800
INFORMATION POR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 909; DB 4;
100.0%; Pred. No. 3.4e-90;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-525-940-23
; Sequence 23, Application US/08525940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 293 amino acids
                                                                                                                                                                             Sequence 2, Application US/09290333
Patent No. 6316222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Best Local Similarity
Matches 166; Conserve
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                               RESULT 4
US-09-290-333-2
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685 INSCVIHCPDGSYQDIKKNLCRKCSENC----KICIEFHNCTECRDGLSLQGSRCSVSC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 TGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAF-----CR-----SLSC 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Frankland Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                            Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.1%; Score 82.5; DB 2; Length B Best Local Similarity 26.0%; Pred. No. 1.5; Matches 27; Conservative 10; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.1%; Score 82.5; DB 2; Length 8 Best Local Similarity 26.0%; Pred. No. 1.5; Matches 27; Conservative 10; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFMED 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 RKEQGKFYDHLLRDCISCASIC----GQHPKQC----AYFCEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 80203

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2848-11-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08976838 Patent No. 5981259 GENERAL INFORMATION:
                     NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TVPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: CONDELL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-023
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 annino acids
     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-525-940-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-976-838-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-976-838-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603 INSCVIHCPDGSYQDIKKNLCRKCSENC----KTCIEFHNCTECRDGLSLQGSRCSVSC 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAF...-CR-----SLSC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.1%; Score 82.5; DB 2; Length 799; Best Local Similarity 26.0%; Pred. No. 1.3; Matches 27; Conservative 10; Mismatches 34; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Franzusoff, Alex
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda. Luls R.
APPLICANT: Miranda. Luls R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
TUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Sulte 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 RKEQGKFYDHLLRDCISCASIC----GQHPKQC----AYFCEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFMED 697
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
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SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRIY APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                   FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONNEL!, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08525940 Patent No. 5866351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colorado : U.S.A.
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: COLO COUNTRY: U. ZIP: 80203
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COUNTRY:
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Scattle
STATE: Washington
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ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/POCKET NUMBER: 2848
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-976-838-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                           CITY: Denver STATE: Colora
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                                685 INSCYTHCPDGSYQDTKKNLCRKCSENC----KTCTEFHNCTECRDGLSLQGSRCSVSC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       719 INSCVIHCPDGSYQDTKKNLCRKCSENC----KTCTEFHNCTECRDGLSLQGSRCSVSC 773
27 TGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAF----CR-----SLSC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Franciscoff, Alex
APPLICANT: Franciscoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
APPLICANT: Wolf, Joseph R.
APPLICANT: Wolf, Joseph R.
APPLICANT: Wolf, Joseph R.
APPLICANTION: ENCODING SAID PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Indels
                                                                                                                             740 -- EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFMED 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 RKEQGKFYDHLLRDCISCASIC----GQHPKQC-----AYFCEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFMED 813
                                                                                            72 RKEQGKFYDHLLRDCISCASIC----GQHPKQC-----AYFCEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.1%; Score 82.5; Di
26.0%; Pred. No. 1.5;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: us 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: CONNell, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
                                                                                                                                                                                                                                                          Sequence 18, Application US/08525940 Patent No. 5866351 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE DOCKET NUMBER: 2848
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-973
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 26.09
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-525-940-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U ZIP: 80203
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                                                                                                                                                                                                                                   US-08-525-940-18
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Query Match

QQ

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RESULT

719 INSCVIHCPDGSYQDIKKNLCRKCSENC----KTCTEFHNCTECRUGLSLQGSRCSVSC 773 33; Gaps -----SLSC 71 Sequence 18, Application US/08976838
Patent No. 5881259
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCE: 31
CORRESPONDENCE ADDRESS: Length 915; Indels 72 RKEQGKFYDHLLRDCISCASIC----GQHPKQC----AYFCEN 1\$\psi\$6 STATE:
COUNTRY: U.S...
ZIP: 80203
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

""ARE: PatentIn Release #1.0, Version #1.30
"ARE: TATION DATA:
US/08/976,838 27 TGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAF----CR COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 774 -- EDGRYFNG -- QDCQPCHRFCATCAGAGADGCINCTEGYFMED Query Match 9.1%; Score 82.5; DB 2; Best Local Similarity 26.0%; Pred. No. 1.5; Matches 27; Conservative 10; Mismatches 34; US-08-323-474-2
Sequence 2, Application US/08323474
Sequence 2, Application US/08323474
Patent No. 547860
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
TITLE OF INFORMION: NOVEL TYROSINE KINASE
HUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS: ADDRESSEE: Sheridan Ross P.C. STREET: 1700 Lincoln St., Suite 3500

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60 RTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 RTCKERCSG----- OEGCKSYVFCLPDPYGCSCATGWKGLQCNEACH----- PGFYGPDCK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                     203 FTRLIVRRC-EAQKWGPECNHLCTACMNNGVCHEDTGECICPPGFMGRTCEKACELHTFG 261
                                                                                                                                                                                                                                                                                                                                                                                        --SCKTICN-HQSQ 59
                                                                                                                                                                                                                                                                                                                                       63; Indels 44;
                                                                                                                                                                                                                                                                                Query Match 8.9%; Score 81; DB 5; Length 1124; Best Local Similarity 24.2%; Pred. No. 2.9; Matches 39; Conservative 15; Mismatches 63; Indels A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. L. Mensens, Marc J. Lauwerys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yees R. Laroche, Laurent S. Jespers,
APPLICANT: Yennick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 RORSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 LRCSC---NNGEMCDRFQ-----GCLCSPGWQGLQCEREGI 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTROL AFFILICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIPICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                        26 WTGVAMRSCPEEQYWDP----LLGTCM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/08465380 Patent No. 5863894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                            TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
       (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
PROFILE OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyot
                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-06093-2
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                  AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-465-380-21
          TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 RICKERCSG----DEGCKSYVFCLPDPYGCSCATGWKGLQCNEACH-----PGFYGPDCK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Indels 44; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 8.9%; Score 81; DB 1; Length 1124; Best Local Similarity 24.2%; Pred. No. 2.9; Matches 39; Conservative 15; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 LRCSC---NNGEMCDRFQ-----GCLCSPGWQGLQCEREGI 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 RQRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06093
FILING DATE: 19930625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
PCT-US93-06093-2
; Sequence 2. Application PC/TUS9306093
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 WTGVAMRSCPEEQYWDP----LLGTCM----
                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,600
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,600
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 75682
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1124 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washingt
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1
CLASSIFICATION:
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11; Gaps ---- EQGKF 78

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27 TGVAMRSCPE--EQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSL4CRK-----EQGKF 78
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; Score 79.5; DB 2; Length 98;
; Pred. No. 0.19;
11; Mismatches 34; Indells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98;
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                                                                                       27 TGVAMRSCPE - - EQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCRK -
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwercys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yes R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 79.5; DB 2; 28.2%; Pred. No. 0.19; tive 11; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIPECATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 213/269
FELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Ancyclostoma caninum US-08-486-397-21
                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08486397
Patent No. 5866542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
      8.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                | :: ||: | 11
77 RDTVIGDCVK-EEECDQH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         79 YDHLLRDCISCASICGQH 96
      Query Match
Best Local Similarity 28.2%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.7%
Best Local Similarity 28.2%
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: L
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH:
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                                                                                                                                                                                                                                                                                          19 TRIVRKAYPECGENEWLDVCGTKKPCEAKCSEEEEED--PICRSFSCPGPAACVCEDGFY 76
                                                                                                                                                                         Length 98;
                                                                                                                                                                                                             34; Indels
                                                                                                                                                                    ; Score 79.5; DB 2;
; Pred. No. 0.19;
11; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
TITLE OF INVENTION: COAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEORGE P. VLASUK; PATRICK ERIC
HUGO STANSSENS; JORIS HILDA
LIEVEN MESSENS; MARC JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAUWEREYS; YVES RENE LAROCHE;
LAURENT STEPHANE JESPERS; and
YANNICK GEORGES JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-UN-1995
CLASSIFICATION OBTA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 203/290
FILICONNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-480-478-49
; Sequence 49, Application US/08480478
; Datent No. 5864009
; GENERAL INFORMATION:
                                                                                       Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street.
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                    8.7%;
ilarity 28.2%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                              77 RDTVIGDCVK-EEECDQH 93
                                                                                                                                                                                                                                                                                                                                   79 YDHLLRDCISCASICGQH 96
                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GANSEMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
      amino acid
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
GY: linear
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                         TOPOLOGY:
                                                                                       ORGANISM:
                                                                                                                                                                    Query Match
Best Local Simi
Matches 22;
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US-08-480-478-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                      US-08-465-380-21
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APPLICANT:
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4

11; Gaps

qq

Qy Dp

Search completed: June 25, 2002, 16:12:13 Job time: 53 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 25, 2002, 16:13:25; Search time 52.94 Seconds (without alignments) 121.609 Million cell updates/sec Run on:

US-09-854-864-16 405 Title: Perfect score:

1 CPEEQYWDPLLGTCMSCKTI......DCISCASICGQHPKQCAYFC 67 Sequence:

Scoring table:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	furin (EC 3.4.21.7	hypothetical prote	variant-specific s	serine proteinase	subtilisin-like pr		subtilisin-like pr	beta-1 integrin su	PACE4A - mouse (fr		conserved hypothet	protein-tyrosine k	integrin beta-1 ch	fibronectin recept	subtilisin-like pr	subtilisin-like pr	TNF receptor assoc	epidermal growth f	STIG1 protein - co	surface protein 51	laminin alpha-1 ch	epidermal growth f	laminin alpha-2 ch	B-cell maturation	gene PACE4 protein	hypothetical prote	protein C16A3.6 [i	protein-tyrosine k	protein-tyrosine k
SUMMARIES	ΩΙ	T43251	H69834	T28626	S34583	JC5571	A39490	JC5570	I46059	152527	A43434	AD0715	158388	S01659	IJMSFB	G02428	JC6148	I61512	JC4387	S46368	T28669	MMKSA	A53183	ММНОМН	S43486	153282	T03869	A88481	154237	JN0712
	DB	7	~	7	~	7	-	7	7	~	~	~		7		7	~	~	7	7	~	-	7	7	7	7	~	7	7	г
	Length 1	1299	108	2664	1548	962	696	975	773	932	1680	108	1124	198	799	668	915	501	1339	146	2233	3084	1210	1751	184	937	248	1119	1122	1123
o f	Query	20.1	19.8	19.0	18.5	18.4	18.4	18.4	17.7	17.7	17.7	17.5	17.3	17.2		17.0	17.0	16.9	16.8	16.7	16.7	16.7	16.5	16.5	16.4	16.4	16.3	16.3	16.3	16.3
	Score	81.5	80	77	75	74.5	74.5	74.5	71.5	71.5	71.5	7.1	70	69.5	69.5	69	69	68.5	89	67.5	67.5	67.5	29	29	66.5	66.5	99	99	99	99
	Result No.	П	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

| | | | : 1171 GVTNSTPPTDCCH 1183

Db

7

H69834

hypothetical protein yhjQ - Bacillus subtilis
C.Species: Bacillus S.Species: I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber S.Stunst, F.; Ogasawara, N.; Moszer, I.; Albertini, B.; Capuano, V.; Carter, N.M.; A.; Enrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y; Fuma, S.; Galizzl, A.; Gal A.Authors: Lauber, J.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau A.Authors: Lauber, S.; Schroeter, B.; Roche, B.; Rosee, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

 protein-tyrosine k hypothetical prote hypothetical prote hypothetical prote epidermal growth f pyruvate ferredoxi hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical are hypothetical protein kinase-related tra kinase-related tra laminin alpha-2 ch hypothetical protein	integrin beta-1 ch variant-specific s eclosion hormone -	ne proprotein convertase; se change 11-Jan-2000	FURIN from Spodoptera frugi	cessing of proproteins with spe Length 1299;	A-2; hes 33; Indels 13; Gaps 3; hes Struckeokerybhlerdciscasic 56 FSCTTCSRPLRIDRINNQCVPCCSER 1170
JH0771 GGHUB T50635 T33697 A27131 B97208 T27786 T27786 JC4126 B48225 A36223 A36223		acid c . armyw	Library, January 1996 functional characterization of F slated from GB/EMBL/DDBJ 8888; NID:g1167859; PID:e219699;	the endoproteolytic prototeinase Score 81.5; DB 2;	υια
666 166.3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	64.5 15.9 798 64.5 15.9 3006 64 15.8 97	3.4.21.75) - fall e names: paired ba Spodoptera frugip -Jan-2000 #sequenc n: T43251 M.; Klenk, H.	he EMBL Data Cloning and mber: Z22368 43251 iminary; tran e: mRNA 1299 <cie> nces: EMBL:Z6</cie>	A: Experimental source: clone Sturin C:Function: A:Description: responsible for the C:Keywords: hydrolase; serine prot Query Match	22; Conservative 22; Conservative EEQYWDPLGTCMSCKTIC :

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Similarity
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                                                                                                     21;
                                                     Query Match
Best Local S
Matches 21
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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Minters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, R. A; Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033
A; Accession: H69834
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                             A;Residues: 1-108 (MUN)
A;Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12900.1; PID:e1183062;
B;Experimental source: strain 168
C;Genetics:
A;Gene: yhjq
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A; Residued: 1-1548 <NAK>
A; Cross-references: GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C; Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C)Accession: T26656
R:Su, X.Z.; Heatwole, V.M.; Werthelmer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D
R:Su, X.Z.; Heatwole, V.M.; Werthelmer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D
A;Title: The large diverse gene family var encodes proteins involved in cytoadherence a
A;Reference number: 220487; MUID:95330813
A;Accession: T26656
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC6,
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R;Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of
                                                                                                                                                                                                                                                                                                                                                                                                        4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variant-specific surface protein 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-2664 <SUX>
A;Cross-references: EMBL:L40609; NID:g886376; PID:g886378; PIDN:AAA75398.1
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQYSEACIEACIDCMKACNHCFTKCLEESVQHHLSGCIRLDRECADICALAVKAMQTDSP
                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                           Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                      25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------CRKEQGKF-YDHLLRDCISCASICGQHPKQC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1031 FC--KEQSRLYEELLRDCGSCTTGKCNNDKCAKCDKQC 1066
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                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                              0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 77; DB 2
Pred. No. 9.5;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: $34583; MUID:93327934
A; Accession: $34583
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22.6%;
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A;Introns: 2197/3
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Best Local Simi
Matches 17;
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Best Local 9
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Subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - N; Alternate names: kexin homolog C; Species: Homo sapiens (man) C; Date: 10.5ep-1999 #text_change 31-Mar-2000 C; Accession: A39490 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000 C; Accession: A39490 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000 A; Aritle: Identification of a second human subtilisin-like protease gene in the fes/fp A; Reference number: A39490; MUD:92075167 A; Areference number: A39490; MUD:92075167 A; Ascession: A39490 A; Ascessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PACE4E is an active processing protease contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: DDBJ:D87994; NID:g2330550; PIDN:BAA21792.1; PID:g2330551
A; Experimental source: brain cerebellum
C; Comment: This enzyme is a processing protease and responsible for processing of of it is retained intracellularly.
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                                                                                                                                                                                                                                                                                                                       1152 CAAVEYWDEGSHRCQPCHKKCSRCSGPSEDQCYTCPRETFLLNTTCVKEC---PEGYHTD 1208
                                                                                                                                                                                                                   -QRTCAAFCCRKEQGKFYD 43
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C;Genetics:
A;Gene: GDB:PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Map position: 15q26-15q26
C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Reywords: glycoprotein; hydrolase; serine proteinase
C; Reywords: glycoprotein; hydrolase; serine predicted <SIG>
F; 1-62/Domain: signal sequence #status predicted <PRO>
F; 196-434/Domain: propeptide #status predicted <PRO>
F; 196-434/Domain: subtilisin homology <SBT>
F; 396-954/Domain: subtilisin homology <SBT>
F; 205, 246, 347, 420/Active site: Asp, His, Asn, Ser #status predicted
F; 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 74.5; DB 2; Length 962; 27.8%; Pred. No. 8.4;
     Length 1548;
                                                                                                         34; Indels
     5
                                                       ed. No. 10;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
Score 75;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: JC5571
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-962 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1209 KDSQQCVLCHSSCRTCEGPHSMQC 1232
                                                                                                         2;
                                                                                                                                                                                                                   1 CPEEQYWDPLLGTCMSCKTICNHQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                 44 HLLRDCISCASIC----GQHPKQC
18.5%;
25.0%;
                                                                                                               Conservative
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Matches 15; Conservative
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4

Gaps

7;

Indels

29;

Length 773;

DB 2;

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PACE4A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
    A;Cross-references: EMBL:U10865; NID:9520520; PIDN:AAA80571.1; PID:9520521
C;Superfamily: integrin beta chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 DCSLGTTSCMAVNGQICNGRGVCECGA--CKCTDPKFQGPTCEMCQTGLGVCAEHKECVQ 625
                                                                                                                                                                                                                                                                                                                                                                                DPLLGT--CMSCK-TICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISdASICGQHPK--Q 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A;Title: PACE4A is a ubiquitous endoprotease that has
A;Reference number: 152527
                                                                                                                                                                                 Score 71.5; DE pred. No. 14; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.78; 29.68;
                                                                                                                                                                                 Query Match
Best Local Similarity 32.8%;
Matches 21; Conservative
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A; Residues: 1-932 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I52527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: 152527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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Best Local Simi
Matches 16;
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152527
PACE4A - mouse (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               626 CRAF
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C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession. JC5570
R; Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na J. Biochem. 121, 941-948, 1997
A; Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing A; Reference number: JC5570; MUID:97335942
A; Accession: JC5570
A; Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Bos primigenius turns (cattle)
C;Species: Bos primigenius turns (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C;Accession: 146059
C;Accession: 146059
Biol. Reprod. 53 153-165, 1995
A;Title: Fibronectin receptors in preimplantation development: cloning, expression, and A;Reference number: 146059; MUID:95399478
A;Accession: 146059
A;Accession: I46059
A;Accession: I74059
A;Acc
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E. Experimental source: brain cerebellum
C; Comment: This enzyme is a processing protease and responsible for processing of variouch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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A.Map position: 15q26-15q26
C.Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C.Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C.Steywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F.16-62/Domain: signal sequence #status predicted <SIG>F.53-149/Domain: subtilisin homology <SERP>F.56-444/Domain: subtilisin homology <SERP>F.55-568/Domain: hydrophobic claster #status predicted <HGL>F.205.246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F.259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                             A Map position: 15q26-15q26
C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Seywords: alternative splicing; hydrolase; serine proteinase
F; 150-969/Product: serine proteinase PCE4 #status predicted <SIG>
F; 196-434/Domain: subtilisin homology <SBT>
F; 205, 246, 420/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 CMSCKT-ICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISC---ASICGQHPKQC 63
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 CMSCKT-ICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISC---ASICGQHPKQC
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74.5; DB 1;
Pred. No. 8.4;
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Pred. No. 8.4;
9; Mismatches
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beta-1 integrin subunit - bovine (fragment)
GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%;
27.8%;
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ilarity 27.8%;
Conservative
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Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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similar but not identical subst
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furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M94375; NID:g157461; PID:g157462 | A:Note: sequence extracted from NCBI backbone (NCBIN:111)933, NCBIP:111934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D50060; NID:9769700; PIDN:BAA08777,1; PID:9769701
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F;172-410/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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C.Superfamily: subtilisin homology
C.Superfamily: subtilisin homology
S.Keywords: hydrolase; serine proteinase; transmembrane proteinase; proteinase; proteinase; serine proteinase; s
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Pred. No. 16;
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Pred. No. 23;
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R; Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.;
J. Biol. Chem. 267, 17208-17215, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.78;
32.18;
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Matches 18; Conserv
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us-09-854-864-16.rpr

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C; Species: Mus musculus (house mouse)
C; Date: 31-Mar.1990 #sequence_revision 31-Mar.1990 #text_change 23-Jul-1999
C; Accession: PLO104; B60597
B; Holers, V.M.; Ruff, T.G.; Parks, D.L.; McDonald, J.A.; Ballard, L.L.; Brown, E.J.
J. Exp. Med. 169, 1589-1605, 1989
A; Title: Molecular cloning of a murine fibronectin receptor and its expression during A; Reference number: PLO103; MUID:89235580
                                                                                                                                                                                                                                                                                  carbohydrate (Asn) (covalent) #st
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A) Residues: 1-799 <HOLD>
A) Residues: 1-799 <HOLD>
A) Cross-references: GB:Y00818; NID:950986; PIDN:CAA33272.1; PID:9762977
A) Experimental source: strain BALB/C
A) Note: the CDNA clone was missing the first nucleotide of Met-1
B; Ryseck, R.P. Macdonald-Bravo, H.; Zerial, M.; Bravo, R.
Exp. Cell Res. 180, 537-545, 1989
A) Title: Coordinate induction of fibronectin, fibronectin receptor, tropomyosin, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: SOLGS9
A; Molecule type: mRNA
A; Residues: 1-798 <-TOMA-
A; Residues: 1-798 <-TOMA-
A; Residues: 1-798 <-TOMA-
A; Rote: the authors translated the codon ATT for residue 696 as Leu
C; Superfamily: integrin beta chain; laminin-type EGF-like homology
C; Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein
F; 1-20/Domain: signal sequence #status predicted <-MAT>
F; 21-798/Product: integrin beta-1 chain #status predicted <-MAT>
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FBSS Lett. 238, 315-319, 1988
A;Title: Murine mRNA for the beta-subunit of integrin is increased in BALB/c-3T3
A;Reference number: S01659; MUID:89005707
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C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Aug-1999
C;Accession: S01659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 EAQKWGPECNHLCTACMNNGVCHEDTGECICPPGFMGRTCEKACELHTFGRTCKERCSGQ 271
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         <FN3A><FN3B><FN3C>
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F;447-527/Domain: fibronectin type III repeat homology <FN3
F;542-625/Domain: fibronectin type III repeat homology <FN3
F;538-720/Domain: fibronectin type III repeat homology <FN3
F;52-772/Domain: transmembrane #status predicted <TWM>
F;822-1099/Domain: protein kinase homology <KIN>
F;830-838/Region: protein kinase ATP-binding mctif
F;140,158,399,48,464,560,596,649,691/Binding site: carbohy
F;855,872,964/Active site: Lys, Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 1
Pred. No. 25;
4; Mismatches
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Pred. No. 22;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 EQGKFYDHLLRDCISCASICGQHPKQCAYFC
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29.3%;
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ilarity 26.4%;
Conservative
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Best Local Similarity
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Best Local Simil
Matches 24; C
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                                                                                                                                                                                                                                                                                                                               Conserved hypothetical protein STY1859 [imported] - Salmonella enterica subsp. enterica (Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi (Species: Obate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 (Species) (Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: IS8388
R; 24egler, S.F.; Bird, T.A.; Schneringer, J.A.; Schooley, K.A.; Baum, P.R.
Rocogene 8, 663-670, 1993
A; Title: Molecular cloning and characterization of a novel receptor protein tyrosine kin A; Reference number: IS8388; WUID:93173509
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C;Genetics:
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C.bate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
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A;Molecule type: mRNA
A;Residues: 1-1124 <RES>
A;Cross-references: GB:L06139; NID:g292823; PIDN:AAA61139.1; PID:g292824
C;Genetics:
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                                                  CPEEQYWDPLLGTCMSCKTICNHQSQRTC---AAFCCRKEQGKFY-DHLLRDCISC
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Pred. No. 4.2;
5; Mismatches
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A;Cross-references: GDB:344185; OMIM:600221
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32.3%;
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C; Function:
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A;Molecule type: DNA
A;Residues: 1-108 <PAR>
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Best Local Simi
Matches 21;
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A; Reference number: A60597; MUID:89121031 A; Accession: B60597

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A Molecule type: mRNA
A; Residues: 596-799 (RYS>
A; Residues: 596-799 (RYS>
C; Comment: The receptor is a heterodimer of alpha and beta chains.
C; Comment: The receptor is a heterodimer of alpha and beta chains.
C; Superfamily: integrin beta chain; laminin-type EGF-like homology
C; Keywords: call adhesion; duplication; glycoprotein; heterodimer; receptor; transmembra
C; Keywords: call adhesion; duplication; glycoprotein; heterodimer; receptor; transmembra
F; 1-20, Domain: signal sequence #status predicted (ASI)
F; 21-739/Product: fibronectin receptor beta chain #status predicted (FXT)
F; 730-752, Domain: transmembrane #status predicted (FXT)
F; 730-752, Domain: intracellular #status predicted (FXT)
F; 750-794, 97, 212, 269, 363, 406, 417, 482, 521, 585, 670, Minding site: carbohydrate (Asn) (covalent)
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GTCMSCK-TICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISCASICGQHPK--QCAYF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C;Keywords: hydrolase; serine proteinase F;148-386/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.0%; Score 69; DB 2; Length 899; Best Local Similarity 26.0%; Pred. No. 27; Matches 19; Conservative 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.5; DB 1;
Pred. No. 22;
8; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.2%;
Best Local Similarity 29.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765 G--QDCQPCHRFC 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 HLLRDCISCASIC 56
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Search completed: June 25, 2002, 16:13:26 Job time: 126 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 25, 2002, 16:11:20; Search time 52.94 Seconds (without alignments) 92.568 Million cell updates/sec

Run on:

US-09-854-864-6 284 1 MAGQCSQNEYFDSLLHACIP......LTCQRYCNASVTNSVKGTNA 51 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMARTES

		đ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	, CI	Description
				1		
Н	284	100.0	184	7	S43486	B-cell maturation
7	74.5	26.2	1101	7	T16840	hypothetical prote
ю	70.5		1548	7	S34583	serine proteinase
4	69.5	24.5	5376	7	T42215	zonadhesin - mouse
S	99		63	7	S07127	chymotrypsin/elast
9	99		330	7	T25169	hypothetical prote
7	65.5	23.1	1299	~	T43251	furin (EC 3.4.21.7
œ	62.5	22.0	666	~	T19275	hypothetical prote
O	62.5	22.0		7	T23681	hypothetical prote
10	61.5	21.7		7	S60231	gibberellin-requla
11	61.5	21.7		7	T24856	hypothetical prote
12	61.5	21.7		7	G88846	protein T12A7.2 [i
13	60.5	21.3		7	T13954	MEGF6 protein - ra
14	60.5	21.3		7	T14119	seven-pass transme
15	59	20.8		7	T15577	hypothetical prote
16	59	20.8		Н	A45558	epidermal growth f
17	58.5	20.6		7	T28675	alpha-51D immobili
18	58.5	20.6		7	T28674	alpha-51D-immobili
19	58	20.4		~	268960	laminin alpha-4 ch
20	57.5	20.5		7	A43434	furin (EC 3.4.21.7
21	57	20.1		7	T20130	hypothetical prote
22	57	20.1		7	G96675	
23	S	20.1		7	T20125	_
24	56.5	19.9		~	S62460	
25	26	19.7		~	A96639	protein T1F9.18 [i
26	99	19.7		~	T34022	zonadhesin - pig
27	S	19.7		7	T22759	hypothetical prote
28	55.5	19.5	339	-	KHRTB	_
29	55.5	19.5		7	T31887	hypothetical prote

hypothetical prote	hypothetical prote	hypothetical prote	S-receptor kinase	hypothetical prote	hypothetical prote	cathepsin B (EC 3.	hypothetical prote	hypothetical prote	finger protein YJL	hypothetical prote	hypothetical prote	vascular endotheli	membrane glycoprot	protein kinase C (alpha tectorin - m	
T31888	T31889	T31898	T05754	T01519	T23682	KHMSB	T27297	T27424	S46625	T27283	T27303	S69207	JC5486	JC1480	T30197	
~	~	~	Н	N	~	Н	7	7	7	7	7	7	7	٦	7	
388	438	445	815	686	294	339	474	552	758	1620	392	419	493	592	2155	
19.5	19.5	19.5	19.5	19.5	19.4	19.4	19.4	19.4	19.4	19.4	19.2	19.2	19.2	19.2	19.2	
55.5	55.5	55.5	55.5	55.5	52	52	52	55	52	52	54.5	54.5	54.5	54.5	54.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

n _change 21-Jul-2000 in, C.J.; Tsapis, A. B lymphoid maturation, is bid	PIDN:CAA83690.1; PID:9471245 , J.C.; Berger, R.; Larsen, C.J.; Tsapi fused to the interleukin 2 gene by a t(IDN:CAA78679.1; PID:929408	ength 184; Indels 0; Gaps 0; VKGTNA 51 VKGTNA 54 L_Change 20-Sep-1999
RESULT 1 S4346 B-cell maturation factor - human N;Alternate names: BCM protein; BCMA protein; BEL protein C;Species: Homo sapiens (man) C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2 C;Accession: S43486; S31208; S3661 R;Laabi, Y; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, Nucleic Acids Res. 22, 1147-1154, 1994 A;Title: The BCMA gene, preferentially expressed during B lymphoid matur A;Reference number: S43486; MUID:94218235 A;Accession: S43486 A;Status: preliminary A;Redevence type: DNA A;Redevence type	L:229574; NID:9471244; ; Carbonnel, F.; Brouet 1992 M, on chromosome 16 is 208; MUID:93010984 L:214954; NID:929407; P L:214955 :135977; OMIM:109545 -16p13.1 cell maturation factor	Query Match 100.0%; Score 284; DB 2; Length 184; Best Local Similarity 100.0%; Pred. No. 8.2e-25; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 MAGQCSQNEXFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNA 51

pr

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furin (EC 3.4.21.75) – fall armyworm
N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; se
                                                                                                                                                                                                                                                                                                                                                              C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S07127
C;Accession: S07127
C;Accession: Biochem. Biophys. 232, 143-161, 1984
A;Title: The isothhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the A;Reference number: S07127; MUID:84255715
A;Reference number: S07127
A;Status: preliminary
A;Rolecule type: protein
A;Residues: 1-63 <BAB>
C;Superfamily: roundworm trypsin inhibitor
                                                                                                                            ä
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25I69
R;Wilkinson, J.
R;Wilkinson, J.
R;Wilkinson, J.
A;Reference number: 21990
A;Ression: T23I0 <WILL>
A;Ression: T23I0 <WILL>
A;Ression: CESP:T23F1.6
C;Genetics:
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                          Length 5376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSQNEYFDSLLHACIPCQLRC -- SSNTP-PLTCQR-YCNASVTNSVKGTN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGPNEVWTE----CTGCEMKCGPDENTPCPLMCRRPSCECSPGRGMRRTN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CSQNEYFDSLLHACIP----CQLRCSSNTPPL---TCQRYCNASVTNSVKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 2; Length 63;
Pred. No. 0.93;
7; Mismatches 18; Indels
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Indels
                                                                                                                         16;
                                                                                                                                                                                                      3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
                                                                            DB 2;
                                                                                                                                                                        38
                                                                                                                                                                                                                                                                                                                                            chymotrypsin/elastase inhibitor - common roundworm
                                                                                                                                                                        4 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 2
Pred. No. 3.8;
8; Mismatches
                                                                                                                         5; Mismatches
                                                                          Score 69.5;
Pred. No. 16;
                                                                       24.5%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.2%;
ilarity 34.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.2%;
Best Local Similarity 28.3%;
Matches 15; Conservative
                                                                                                                         14; Conservative
    C; Keywords: cell adhesion
                                                                          Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:T23F1.6
A;Map position: 5
A;Introns: 16/3
C;Superfamily: gliadin
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Ridgo, Z.; Garbers, D.L.

J. Blol. Chem. 273, 3415-3421, 1998

A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro
A;Reference number: Z22080; MUID:98123114

A;Accession: T42215
A;Actuus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5376 <GAO>
                                                                                                                       A; Residues: 1-1101 <GEI>
A; Residues: 1-1101 <GEI>
A; Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 «NAK>
A;Cross-references: GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                             A;Gene: CESP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S34583
R;Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, A;Reference number: S34583; MUID:93327934
A;Accession: S34583; MUID:93327934
                                                                                                                                                                                                                                                                                                                                                                                                                  'n
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: sperm-specific membrane protein
C;Species: Mus muscullus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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د.
                                                                                                                                                                                                                                                                                                                                                                   Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: functions in multiple cell adhesion processes A; Note: found exclusively on the apical region of the sperm head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 QCSQSTVFNSDLNVCVPLAIQNSCDSSTQQPVCS--C-SQVSSSCPGTS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 QCSQNEYFDSLLHACIPCQLR--CSSNTPPLTCQRYCNASVTNSVKGTN 50
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 QCSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQRYCNASVTNSVK
                                                 elegans cosmid T10E10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                              Score 74.5; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70.5; DB
Pred. No. 4.4;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
R;Geisel, C. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            υ,
.,
                                            A; Description: The sequence of C. A; Reference number: Z18588
A; Accession: T16840
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34.7%;
                                                                                                                                                                                                                                                                                                                                                              26.2%;
                                                                                                                                                                                                                                                                                                                                                         Query Match 26.2%
Best Local Similarity 36.7%
Matches 18. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zonadhesin - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: Zan
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A;Title: GASA, a gibberellin-regulated gene family from Arabidopsis thaliana related A;Reference number: $60229; MUID:95244835
A;Accession: $60231
A;Accession: S60231
A;Accession: S60231
                                                                                 A.Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Gross references: EMBL:281573; PIDN:CAB04625.1; GSPDB:GND0020; CESP:M0269.1
A;Experimental source: clone M0269
C;Genetics:
C;Genetics:
A,Gene: CESP:M0269.1
A,Gene: CESP:M0269.1
A,Gene: CSP:M0269.1
A,Gene: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z73911; PIDN:CAA98142.2; GSPDB GN00022; CESP:T12A7.2 A;Experimental source: clone T12A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GASA3
C;Superfamily: gibberellin-regulated protein GASA2
E;1-18/Domain: signal sequence #status predicted <SIG>
F;19-99/Product: gibberellin-regulated protein GASA3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T12A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gibberellin-regulated protein GASA3 precursor - Arabidopsis thaliana
NiAlternate names: GAST1 protein homolog
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL:U11764; NID:g887934; PIDN:AAB06308.1; PID:g887935 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61.5; DB 2;
Pred. No. 4.4;
7; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                   5,
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A; Reference number: 219943
A; Accession: T24856
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      DB
      submitted to the EMBL Data Library, November 1996 A;Reference number: 219781 A;Accession: T23681
                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.5; DI
Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 DSLLHAC-IPCQLRC-SSNTPPLTCQRYCNASV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S60231
R;Herzog, M.; Dorne, A.M.; Grellet, F.
Plant Mol. Biol. 27, 743-752, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%;
35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.0%;
Best Local Similarity 35.8%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.69
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA A; Residues: 1-99 <HER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP:T12A7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T24856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                   Cincession: T43251

Richellik, M.; Klenk, H.

Submitted to the EMBL Data Library, January 1996

A; Description: Cloning and functional characterization of FURIN from Spodoptera frugiper A; Reference number: 222368

A; Reference number: 222368

A; Accession: T43251

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-1299

A; Cross-references: EMBL: Z68888; NID: 91167859; PID: e219690; PIDN: CAA93116.1
                                                                                                                                                                                                                                                                                                                                                                               C;Function:
A;Description: responsible for the endoproteolytic processing of proproteins with specif
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 3
A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Submitted to the EMBL Data Library, September 1994
S.Babmitted to unaber: 219099
S.Reference number: 219099
S.Accession: T19275
S.Actus: preliminary; translated from GB/EMBL/DDBJ
S.Katus: preliminary; translated from GB/EMBL/DDBJ
S.Residues: DNA
S.Residues: 1-999 < WILL>
S.Coss-references: EMBL: 237139; PIDN: CAA85494.1; GSPDB: GN00021; CESP: F34D10.2
S.Experimental source: clone C14B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:234799; PIDN:CAA84320.1; GSPDB:GN00021; CESP:F34D10.2 A;Experimental source: clone F34D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23681
R;Matthews, L.
C;Specfes: Spodoptera frugiperda (fall. armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z68888; NID:91167859; PID:e219690; PIDN:CAA93116.1
A;Experimental source: clone Sfurin 6; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1150 CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65.5; DB 2; Length 1;
Pred. No. 14;
8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F34D10.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516 YEDSLIKTCIGRAFERVKKMTPPLRIQSYFVSSTPNGLDG 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rikershaw, J.

Submitted to the EMBL Data Library, June 1994
A;Reference number: 219464
A;Accession: T21723
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molécule type: D12>
A;Residues: 1-999 <W12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62.5; i
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.1%;
Best Local Similarity 34.0%;
Matches 18; Conservative
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Best Local Similarity 42.5%;
Matches 17; Conservative
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Seven pass transmembrane receptor protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T1419
C;Accession: T14119
C;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C23G10.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dace: 20.5ep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T15577
R;Latreille, P.
R;Latreille, P.
A;Reference number: 218372
A;Bescription: The sequence of C. elegans cosmid C23G10.
A;Reference number: 218372
A;Recession: T15577
A;Accession: T15577
A;Accession: T1557
A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001 QCKENYYKPPAQDACLPCDCFPHGSHSRACDMDTGQCACKPGVIGRQCNRCDNPFAEVTS 2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQ-----RYCN-----ASVTN 44
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A;Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60.5; DB 2;
Pred. No. 1e+02;
5; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 25, 2002, 16:13:20 Job time: 120 sec
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ilarity 28.3%;
Conservative
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ESVFHPLYPAEIRCSADGPPL
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Best Local Similarity 42.9
Matches 9; Conservative
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Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Celsr1
A;Map position: 15
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C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Space: C:Date: ID-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: G88846
R:anonymous, The C. elegans Sequencing Consortium.
S:Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger ac.uk/Projects/C_eleA:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:chr_IV; PIDN:CAA98142.1; PID:g3879789; GSPDB:GN00022; CESP:T12A7.
C;Genetics:
A;Gene: T12A7.2
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C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C.Accession: T19954
R.Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: 214126; MUID:98360089
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A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6
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                                                                                                                                     Length 483;
A; Introns: 36/3; 71/1; 146/1; 255/2; 287/2; 340/3; 387/1; 449/2
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                                                                                                                                 Score 61.5; DB
Pred. No. 17;
5; Mismatches
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Pred. No. 59;
8; Mismatches
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A; Residues: 1-520 <STO>
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Length 3034;

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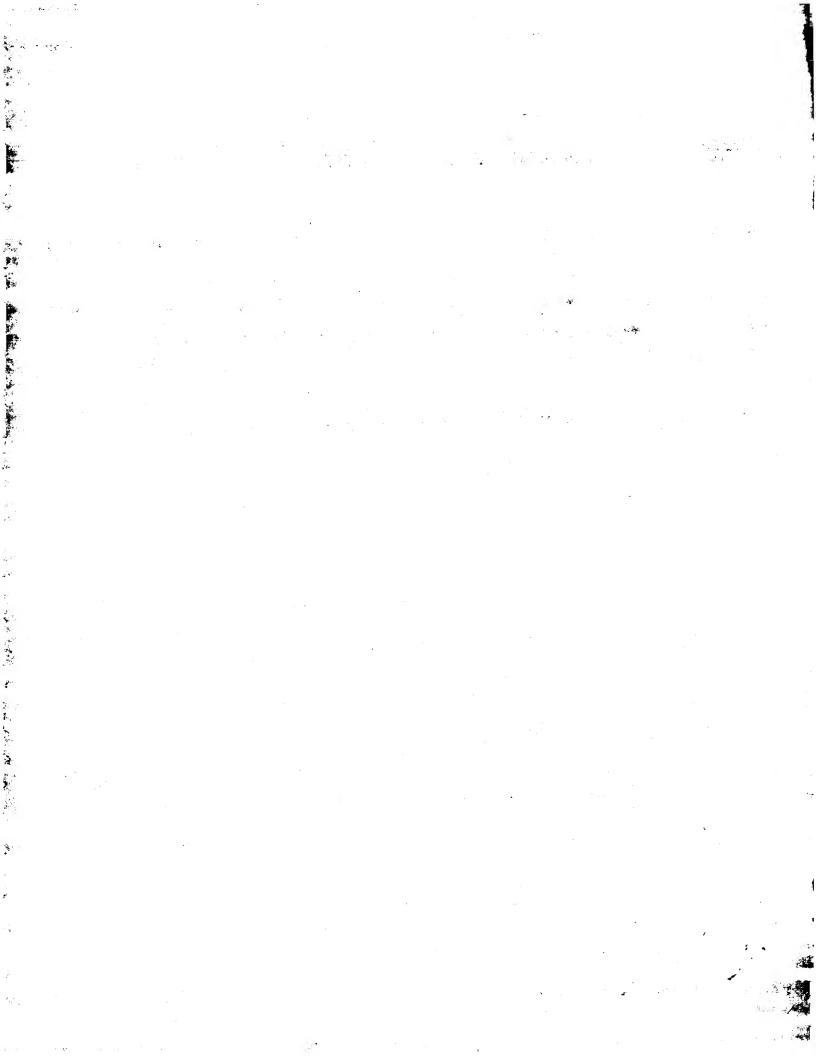
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14

RESULT

Length 758

us-09-854-864-6.rpr



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 25, 2002, 16:12:15; Search time 27.55 Seconds (without alignments) 71.677 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-854-864-6 284 1 MAGQCSQNEYFDSLLHACIP......LTCQRYCNASVTNSVKGTNA 51

Scoring table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q02223 homo sapien	mus	mus	P07851 ascaris suu	-	P46687 arabidopsis		_		-			Q28983 sus scrofa	P00787 rattus norv	O15230 homo sapien		P92127 giardia lam		P42124 drosophila		_	Q63358 rattus norv	Q9qy06 mus musculu	Q13459 homo sapien		shope	Q29537 canis famil		P97430 mus musculu		1 orycto	2536 human	P20872 human immun
SUMMARIES	ID	TR17_HUMAN	PCK5_MOUSE	ZAN_MOUSE	ICE1_ASCSU	SORL_CHICK	GAS3_ARATH	SSPO_BOVIN	LMA4_MOUSE	LMA4_HUMAN	FUR2_DROME	YB40_HUMAN	YAE5_SCHPO	ZAN_PIG	CATB_RAT	LMA5_HUMAN	CATB_MOUSE	VS41_GIALA	YJU6_YEAST	EZ_DROME	VEGC_HUMAN	KPCZ_MOUSE	MY9B_RAT	MY9B_MOUSE	MY9B_HUMAN	TNR6_BOVIN	VT2_SFVKA	P53_CANFA	YLK3_CAEEL	ALX1_MOUSE	TR1A_HUMAN	KPCZ_RABIT	ENV_HV2S2	ENV_HV2ST
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	53 18.7 3075 1 LMA1_HUMAN 52.5 18.5 847 1 YOBS_NDVAC 52.5 18.5 3718 1 LMA5_MOUSE 52 18.3 56 1 ITR4_RADM 52 18.3 14.1 LYEP_DROME 52 18.3 470 1 PROP_CAVPO 52 18.3 470 1 PROP_CAVPO 52 18.3 1062 1 NAL2_HUMAN 52 18.3 1115 1 GPCR_LYNST 52 18.3 1115 1 GPCR_LYNST 52 18.3 1483 1 UFD4_XEAST 52 18.3 1696 1 PCKS_BRACL	ALIGNMENTS	UMAN STANDARD; PRT; 184	U02223; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily member	maturation protein). TNFRSF17 OR BCMA. TNFRSF17 OR BCMA. Homo sapiens (Human). Eukarycta: Metazoa; Chordata; Craniata; Vertebrata Mammalia; Eutheria; Primates; Catarrhini; Hominida	[1] SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION. SEQUENCE-PETIPHERAL BLOOD LEUKOCYTES, AND LYMPH NODE; MEDLINE-93010984; PubMed-1396583; Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Ber Larsen C.J., Tsapis A.; "A new gene, BCW, on chromosome 16 is fused to the by a t(4;16)(q26;p13) translocation in a malignant EMBO J. 11:3897-3904(1992).	AEDLINE-94218235; PubMed-8165126; MEDLINE-94218235; PubMed-8165126; Laabi Y., Gras M., Brouet J., Berger R., Larsen C., The BCMA gene, preferentially expressed during B ly maturation, is bidirectionally transcribed."; Nucleic Acids Res. 22:1147-1154(1994).		[4] [24] [54] [54] [54] [55] [56] [57] [58] [58] [58] [58] [58] [58] [58] [58	FUNCTION. MEDLINE=20363816; PubMed=10903733; MEDLINE=20363816; PubMed=10903733; Hatzoglou A., Roussesl J., Bourgeade M.F., Rogier E., Inoue J., Devergne O., Tsapis A.; TNF receptor family member BCAA.; TNF receptor family member BCAA.; TNF receptor associated factor (TRAF) 1, TRAF2, and activates NF-kappa B. elk-l., c-Jun N-terminal kinase mitogen -activated protein kinase."; J. Immunol. 165:1322-1330(2000).

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FEBS Lett. 327:165-171(1993).
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          MEDLINE=20259066; PubMed=10801128; Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Hartison R., Kindsvogel W., Clegg C.H.; "TACI and BCMA are receptors for a TNF homologue implicated in B-cell autoimmune disease.";
                                                                                                           -1- FUNCTION: RECEDED for TNFSF13B/BLyS/BAFF.
-1- TISSUE SPECIFICITY: EXPRESSED IN MATURE B-CELLS.
-1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCK5_MOUSE STANDARD; PRT; 1877 AA.

004552; 062040;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(Convertase PC5) (Subtilisin-like proprotein convertase 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa T., Murakami K., Nakayama K.;
"Identification of an isoform with an extremely large Cys-rich region
of PC6, a_Kex2-like processing endoprotease.";
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                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Proto-oncogene; Transmembrane; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 284; DB 1; Length 184; 100.0%; Pred. No. 1.9e-27; ive 0; Mismatches 0; Indels (
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277AF11E2767D932 CRC64;
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                                                                                                                                                                 WHICH INVOLVES BCMA AND IL2
                                                                                                                                                                                                                                                                                                                                        , AB052772; BAB60895.1; -. S31208; S31209; S31209.
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EMBL; Z29575; CAA82691.1; --
EMBL; Z29574; CAA82690.1; --
EMBL; U95742; AAB67251.1; --
                                                                                                    Nature 404:995-999(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism.
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                  109545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                             EMBL;
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Matches
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AND PCSA/SHORT; ARE PRODUCED BY ATTERNATIVE SPLICING.

-1 TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE
INTESTINE, ADREBALS AND LOUG BUT NOT IN THE BRAIN.

-1 DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE BRBRYO.

-2 DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE BRBRYO.

-3 DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE BRBRYO.

-4 DEVELOPMENT BY PRESSION OBSERVED IN DIFFERENCIATED DECIDIA. AT
E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENCIATED DECIDIA. AT
E7.5, INTENDES EXPRESSION OBSERVED IN DIFFERENCIATED BETWEEN
NASCENT MESCODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
SAC FOLLOWED BY A CONFINATION TO DERMAMYOTOME COMPARTMENT. BETWEEN
E9.5 AND E11.5, ABUNDANT EXPRESSION IN ARR (FILKEREDE DECIDERAL
CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
TO THE CONDENSING MESENCHYM SURROUNDING THE CARTLIAGE. AT THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rancourt S.L., Rancourt D.E.;
"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";

Dev. Genet. 21:75-81(1997)

-!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSISSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED IN THE CELLGLAR PROLIFERATION OF ADRENAL CORPEX VIA THE ACTIVATION OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-YAA-YAA-RAC-1-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
SUBCELLULAR LOCATION: PCSA IS SCRETED THROUGH THE REGULATED SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARAUCLERR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STACE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL EXPRESSION.
MEDLINE-96293359; PubMed-8698813;
Constam D.B., Calfon M., Robertson E.J.;
"SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis.";
J. Cell Biol. 134:181-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bendayan M., Seidah N.G.;
"The isoforms of proprotein convertase PC5 are sorted to different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93342056; PubMed-8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/Kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
                                                                                                                                                                                                                                                                                          mammalian Kex2-11ke processing endoprotease family: its striking
structural similarity to PACE4.";
J. Biochem. 113:132-135(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
                                                                                                                                                                                                                                                      "Identification and functional expression of a new member of
                                                                                                                                                    Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nonendocrine cells.";
Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION. MEDLINE-97103178; PubMed-8947550;
SEQUENCE FROM N.A. (ISOFORM PC5A).
TISSUE-Brain, and Intestine;
MEDLINE-93224489; Pubmed-8468318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM PC5A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subcellular compartments.";
J. Cell Biol. 135:1261-1275(1996).
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MEDLINE=97436919; PubMed-9291583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Adrenal cortex;
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us-09-854-864-6.rsp

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'ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.
DOMAIN: THE PROPEPTIED DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
                                                            DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING INFORMATION. AC 1 DIRECTS TON LOCALIZATION AND INTEREST WITH THE TGN SORTING PROTEIN PACS-1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Cleavage on pair of basic residues; Repeat; Alternative splicing;
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CELL ATTACHMENT SITE (POTENTIAL)
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CYS-RICH MOTIF (CRM) REGION.
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N-LINKED GECNAC.
N-LINKED GELCNAC.
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Pfam: PF00082; Peptidase_S8; 1.
Pfam: PF00082; Peptidase_S8; 1.
PRINTS: PR00723; SUBTILISIN.
SMART: SM00181; EGF; 3.
SMART: SM00081; EGF. 3.
SMART: SM00081; EGF. 3.
SMART: SM00081; EGF. 3.
PROSITE: PS00136; SUBTILASE_ASP; 1.
PROSITE: PS00138; SUBTILASE_HIS; 1.
PROSITE: PS00138; SUBTILASE_SER; 1.
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EMBL; L14932; AAA74636.1; -
PIR; JX0248; JX0248.
PIR; A48225; A48225.
HSSP; Q99405; IMPT.
MEROPS; S08.076; -
InterPro; IPR00561; EGF-like.
InterPro; IPR0025174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002884; P_domain.
InterPro; IPR000209; Peptidase_S8
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                                                   RETICULUM.
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                      1;
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- 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.
- 1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
- 1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.
- 1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA ON PROMOTING ADHESION TO THE OVIDUCITAL ISTHMUS.
- 1- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
- 1- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
- 1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
- 1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXCLUSIVELY ON THE
                                                                                                                                                                                                      Gaps
                                    GEYIDDQGHCQTCEASCAKCWGPTQEDCISCPVTRVLD
ATEESWAEGGFCMLVKKNNLCQRKVLQQLCCKTCTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a sperm-specific molecule-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao Z., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zonadhesin gene and the human
zonadhesin qene (ZAN).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
   (POTENTIAL)
                                                                                                                                                                                                      .,
2
                     (POTENTIAL)
                                                                                                                                                                  DB 1; Length 1877;
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                                                                                                                                                                                                    22; Indels
                                                                      (IN ISOFORM PC5A).
MISSING (IN ISOFORM PC5A).
MW; EC850E2DF20EA1C3 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                   ZAN_MOUSE STANDARD; PRT; 5376 AA. 088799; 008647; 16-027-2001 (Rel. 40, Created) 16-027-2001 (Rel. 40, Last sequence update) 16-027-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                24.8%; Score 70.5; DB 34.7%; Pred. No. 0.86; Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domains.";
J. Biol. Chem. 273:3415-3421(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Testis;
MEDLINE-98123114; PubMed-9452463;
Gao Z., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97271566; PubMed-9126492;
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1877 AA; 209287
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1733
915
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                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
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878
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                   CARBOHYD
VARSPLIC
                                                                                           VARSPLIC
SEQUENCE
   CARBOHYD
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   FTFFF
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TARAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.

MEDLINE—95006335; PubMed—7922044;

MEDLINE—95006335; PubMed—7922044;

Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;

The molecular structure of the complex of Ascaris

chymotrypsin/elastase inhibitor with porcine elastase.";

CHORTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.

I. STMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.

PIBS: 1EAI: 05-APR-99.

InterPro; IPR002919; TIL.

Serine protease inhibitor; 3D-structure.

This DISULED

THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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P07851;
01-AGG-1988 (Rel. 08, Created)
01-AGG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chymotrypsin/celastes isolnibitor 1 (C/E-1 inhibitor).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae, Ascarididae, Ascaris.
NCBL_TaxID=6253;
                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.5%; Score 69.5; DB 1; Length 5376; 36.8%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDLINE-84255715; PubMed-6564898;
Babin D.R., Peanasky R.J., Goos S.M.;
"The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure.";
Arch. Biochem. Biophys. 232:143-161(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0E44DB77DF2A2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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PROSITE; PS01186; EGF_2; 18.
PROSITE; PS00740; MAM_1; FALSE_NEG.
Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
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                                                    MGD; MGI:106656; Zan.
InterPro; IPR000561; EGF-like.
InterPro; IPR003645; Foln.
                                                                                            InterPro; IPR003645; FOIN.
InterPro; IPR003645; FOIN.
InterPro; IPR00299; MAM.
InterPro; IPR00299; TIL.
InterPro; IPR001907; VWFC.
InterPro; IPR001846; VWd.
Pfam; PF00629; MAM; 3.
Pfam; PF00629; TIL; 25.
Pfam; PF00094; VWd; 4.
SMART; SM00181; EGF; 2.
SMART; SM00214; VWC; 17.
SMART; SM00214; VWC; 17.
SMART; SM00214; VWC; 17.
                     EMBL; U97068; AAC26680.1;
                                            AAC53125.1;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                MOTABLE AND CONTAINED TO THE MENT OF THE MOTABLE AND CONTAINED TO THE MOTABLE AND CONTAINED THE RECEPTOR. INTERLY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES. BINDS LDL, THE MADOR CHOLESSEROL-CERRYING LIPOPROTEIN OF PLASMA, AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS. BINDS THE RECEPTOR-ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK REGULATORY EFFECTS ON THIS RECEPTOR.

1. SUBCELLULAR LOCATION: Type I membrane protein (Potential).

2. SUBCELLULAR LOCATION: Type I membrane protein (Potential).

2. SIMILARITY: CONTAINS 5 BNR REPEATS.

3. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAINS.

4. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Sortilin-related receptor (Sorting protein-related receptor containing
LDLR class A repeats) (SorLA) (SorLA-1) (Low-density lipoprotein
receptor relative with 11 11gand-binding repeats) (LDLR relative with
11 11gand-binding repeats) (LR11) (Fragment).
Eukaryota; Metazoa; Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                    Gaps
                                                                                   8
                                                                                                                    CGPNEVWTE----CTGCEMKCGPDENIPCPLMCRRPSCECSPGRGMRRTN 50
                                                                                                         5 CSQNEYFDSLLHACIPCQLRC--SSNTP-PLTCQR-YCNASVTNSVKGTN 50
                                                        Score 66; DB 1; Length 63;
Pred. No. 0.12;
7; Mismatches 18; Indels
             REACTIVE BOND.
5DC10DE75B375F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002860; BNR.
InterPro; IPR000561; EGF-like.
InterPro; IPR003961; FW_III.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR000033; Ldl_receptor_rep.
                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=97301565; PubMed=9157966;
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                                                          Query Match 23.2%;
Best Local Similarity 34.0%;
Matches 17; Conservative
                         MM.
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SEQUENCE FROM N.A.
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31
63 AA;
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SORL_CHICK
ID SORL_CHICK
AC Q98930;
DISULFID
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Pfam;
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SWART: SW00181; EGF; 1.

SWART: SW00060; FN3; 1.

SWART: SW00192: LDLa.

SWART: SW00135; LY: 5.

SWART: SS01086; EGF_2; 1.

PROSITE: PS011209; LDLRA_1; 11.

PROSITE: PS00068; LDLRA_2; 11.

NON_TER: PS00068; LDLRA_2; 11.

NON_TER: PS00068; LDLRA_2; 11.

NON_TER: PS00068; LDLRA_2; LDLRA_2; LDL; LDLY, LDLY
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LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 7.

LDL-RECEPTOR CLASS A 
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Query Match
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SSPO_BOVIN
DT 01-0CT'
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OC EMARTY
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RN (1)
RR SEQUENT
RA GOBOTO
RA LAMBLIN
RA LAMBLIN
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RX MEDLINE-20083488; PubMed=10617198;

RA MEDLINE-20083488; PubMed=10617198;

RA MEDLINE-20083488; PubMed=10617198;

RA MELTINE-20083488; PubMed=10617198;

RA Harris B., Manorge W., Brandt P., Grivell L.A., Rieger M.,

RA Harris B., Manorge W., Brandt P., Grivell L.A., Rieger M.,

RA Harris B., Manorge W., Brandt P., Grivell L.A., Rieger M.,

RA Harris B., Manorge W., Brandt P., Grivell L.A., Rieger M.,

RA Harris B., Manorge W., Brandt P., Matheler M.,

RA Reichert B., Deftetelle D., Perez-Alonso M., Schmidtheini T.,

RA Reichert B., McUllagh B., Bilham L., Robben M., Schmidtheini T.,

RA Langham S.-A., McCullagh B., Bilham L., Robben M., Bancroft I.,

RA And Mer Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

RA Molzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,

RA Molzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,

RA Molzer E., Brandt A., Peters S., Van Staveren M., Lamberth S., Van den Daele H.,

RA Moniagu M., Rogers J., Cronin A., Quall M., Rayahar R., De Clercq R.,

RA Pan Montagu M., Rogers J., Cronin A., Quall M., Maryahar S.,

RA Doggett J., Hall S., Kay M., Lennard N., McLay K.,

Bertett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,

RA Borkova D., Bloecker H., Scharfer M., Grimm M., Loennert E., Toennert T., H.,

Dosg S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Massenet C., Ouigley F., Clabauld G., Muendlein A., Felber R.,

Rhumann S., Argiriou A., Vialle D., Liquori R., Panorer D., Herzl A.,

Rhumann S., Argiriou A., Vialle D., Muendlein A., Felber R.,

Rhumann S., Argiriou A., Vialle D., Muendlein A., Pelber S.,

Rheidor F., Geber N., Schnidt W., Leber S., Francs P., Blerke C.,

Rhumann S., Argiriou A., Vialle D., Muendlein A., Pelber S.,

Rheidor F., Schwarz S., Scholler E., Johnson D., Joses T.,

Rheidor P., Boeve M., Wilson R.K., de la Bastide M., Habbermann K.,

Rockaria P., Bevan M., Wilson R.K., de la Bastide M., Habber S., Schonking T., Meber S., Scholler M., Abroney S.,

Rheidor P., Courtney L., Cloud J.
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                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gibberellin-regulated protein 3 precursor.
GASA3 OR AT4G09600 OR T25P2-40.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herzog M., Dorne A. M., Grellet F., "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana related to the tomato GAST1 gene."; Plant Mol. Biol. 27:743-752(1995).
                                                                                                                                                       <u>;</u>
                                                                                                        Length 1592;
                                                                                                                                                    18; Indels
                            24EDAA5BA231B203 CRC64;
                                                                                                                                                                                                                                                     1376 GRCSRTEFECOOLHKCIPNWKRCDGRRDCODGTDERSCPTHSSLS 1420
                                                                                                                                                                                                   3 GQCSQNEYFDSLLHACIP----CQLR--CSSNTPPLTCQRYCNAS 41
                                                                                                     DB 1;
                                                                                                                             Pred. No. 7.8;
6; Mismatches
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                                                                                                     Score 62;
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MEDLINE-95244835; PubMed-7727751;
1592 1592
1592 AA; 178409 MW;
                                                                                                21.8%;
                                                                                                   Query Match 21.8
Best Local Similarity 33.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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STRAIN=CV. COLUMBIA;
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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MEDLINE-96338614; PubMed-8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,
Lamalle D., Dastugue B., Meiniel A.,
"SCO-spondin: a new member of the thrombospondin family secreted by
the subcommissural organ is a candidate in the modulation of neuronal
                                                                                                                                                                                                                                                                                                                                               thaliana.";
Nature 402:769-777(1999).
-!- FUNCTION: INVOLVED IN LATE STAGES OF SEED MATURATION, OR IN EARLY
STEPS OF GERMINATION.
STEPS. OF GERMINATION.
Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., Natson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., An P., Zhong J., Preston R., Jones K., Drone K., Cotton M., Joshu C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hammed A., Lodhi M., Johnson A., Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Boyldae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggregation.";
J. Cell Sci. 109:1053-1061(1996).
J. PUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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84549874B08A47FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 GRCSKSSRPNLCLRACNSCCYRCNC-VPPGTAGNHHLCPCYASIT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: SILIQUES AND DRY SEEDS.
-i- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
-i- SIMILARITY: BELONGS TO THE GAST1 FAMILY.
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-2001 (Rel. 40, Last annotation update)
SCO-spondin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.5; DB Pred. No. 0.64; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     867
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35.6%;
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P98167;
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        PROSITE; PSG1285; FA58C_1; 1.
PROSITE; PSG1286; FA58C_2; 1.
PROSITE; PSG109: LDLRA_1; 3.
PROSITE; PS50092; TSP1; 4.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
NON_TER 1 TSP TYPE-1 1.
DOMAIN 26 81 TSP TYPE-1 1.
DOMAIN 103 142 EGF-LIKE 1.
        SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
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N-LINKED (GLCNAC.
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F5/8 TYPE C.
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TSP TYPE-1 4.
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InterPro; IPR002172; LDL_recept_A.
InterPro; IPR002919; TIL.
InterPro; IPR00984; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWFC.
Pfam; PF00754; F5_F8_type_C; 1.
Pfam; PF001826; TIL.
Pfam; PF001826; TIL.
Pfam; PF00099; TSP1.; 4.
 DEVELOPMENTAL STAGE: EMBRYO.
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SMART; SM00231; FA58C; 1.
SMART; SM00192; LDLa; 3.
SMART; SM00209; TSP1; 4.
SMART; SM00214; vwc; 1.
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Score 60; DB 1; Length 867; Pred. No. 7.6;

21.18; 42.98;

Query Match Best Local Similarity

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WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
SUBBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLIGBULES AT EACH END.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 targets of developing sensory axons.";
J. Comp. Neurol. 378:547-561(1997).
-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transitions, and heterotrimeric
                                                                                                                                                                                                                                                                                                                                                                                                             Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R., Sorokin L.M.; "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of endothelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEDLINE-98010627: PubMed-9346933;
Livanainen A., Kortesmaa J., Sahlberg C., Morita T., Bergmann U.,
Theslef I., Trygqavason K.;
"Primary structure, developmental expression, and immunolocalization
of the murine laminin alpha4 chain.";
J. Biol. Chem. 272:27862-27868(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete cDNA coding sequence and tissue-specific expression of the mouse laminin alpha 4 chain.";
Matrix Biol. 15:433-437(1996).
                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND
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                                                                                                                                                                                                                                                                                            Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ICR, TISSUE=Placenta;
MIDELINE=97296337; PubMed=9151674;
Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J.,
Jenkins N.A., Copeland N.G., Sanes J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lentz S.I., Miner J.H., Sanes J.R., Snider W.D.; "Distribution of the ten known laminin chains in
                                                                                                                       LWA4_MOUSE STANDARD; PRT; 1816 AA. P97927; P70409; 088785; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Laminin alpha-4 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C; TISSUE=Endothelial cells; MEDLINE=97363207; PubMed=9219532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 246:727-735(1997).
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MEDLINE=97202462; PubMed=9049981;
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MEDLINE=97187457; PubMed=9034910;
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SEQUENCE OF 836-1106 FROM N.A.
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14 LLHACIPCOLRCSSNTPPLTC
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
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                                                                                                        LMA4_MOUSE
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TISSUE-Fetal lung;

BEDLINE-53300971; PubMed-7781776;

Itvanainen A., Sainlo K., Sariola H., Tryggvason K.;

Primary structure and expression of a novel human laminin alpha 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                  (POTENTIAL)
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( IN REF. 2).
( IN REF. 2).
( IN REF. 1; AA SEQUENCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.1%; Score 60; DB 1; Length 1816;
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B49C45F3A45999D8 CRC64;
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                  REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 15;
10; Mismatches
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Best Local Similarity 23.8%
Matches 15; Conservative
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SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PERIPHERAL NERVES,
TISSUE SPECIFICITY: STRONGLY EXPONA, AORTIC ENDOTHELIUM,
CARDILG MUSCLE, FAT, DERMIS, LUNG STROMA, AORTIC ENDOTHELIUM,
ENDOCARDIUM AND ENDOTHELIUM OF BLOOD VESSELS IN SKIN AND BRAIN.
DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL, STRUCTURE.
SUMMAIN: DOMAIN GI GLOBULAN
SIMILARITY: CONTAINS 3.5 LAMININ EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS0002; EGF_1; UNKNOWN_1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
PROSITE; PS50025; LAM_G_DOMAIN: 5.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-11ke domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAMININ GEF-LIKE 1.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ IN TOTAL 4. (INCOMPLETE).
DOMAIN II AND 1.
LAMININ G-LIKE 3.
COLLED COIL (POTEWTIAL).
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EMBL, V09827; CAA70970.1; --
EMBL, U59865; AAC24725.1; --
EMBL, U69176; AAC3178.1; --
EMBL; U69176; AAC32982.1; --
HSSP POLGA68; IKLO.
HGD, MGT: 109231; Lama4.
InterPro; IPR00049; Laminin_EGF.
InterPro; IPR00049; Laminin_EGF.
InterPro; IPR001791; Laminin_EGF.
Ffam; PF00053; laminin_EGF; 3.
Pfam; PF00054; laminin_G, 4.
SMART; SM00180; EGF_Lam; 3.
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LAMININ EGF-LIKE 3

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1- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG, VARX SMALLA BND LARGE INTESTINES, PLACEMENTA, LIVER; WEAR OR NO EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE, BRAIN. HIGH EXPRESSION IN FETAL LUNG AND KIDNEY. EXPRESSION IN FETAL AND NEWBORN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS IN TISSUES SUCH AS SMOOTH MUSCLE AND DERRIS.

1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT UDMAIN: THE ALPHA-HELICAL DOMAINS I OF FORM A COILED COIL STRUCTURE.

1- DOMAIN: DOMAIN G IS GLOBULAR.

1- SIMILARITY: CONTAINS 3.5 LAMMIN GGFLIKE DOMAINS.

1- SIMILARITY: CONTAINS 5 LAMMIN G-LIKE DOMAINS.

1- SIMILARITY: CONTAINS 5 LAMMIN G-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                    WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFRENT POLYPEPETIDE CHALNS (ALPHA, BETA, GAMMA,), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHARED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
                                                                                                                                                                                                                                                "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of a partial cDNA encoding a variant laminin A chain."; Genomics 22:237-239(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00054; laminin_c, ...
SWART; SW00180; EGF_Lam; 3.
SWART; SW00282; Lam; 5.
PROSITE; PS01022; EGF_I UNKNOWN 1.
PROSITE; PS010248; LAMININ_TYPE_EGF; 3.
PROSITE; PS50025; LAM_G_DOMAIN; 5.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-11ke domain; Cell adhesion; Repeat; Signal.

24.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                 TISSUE=Heart;
MEDLINE-95048381; PubMed=7959779;
Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
                 MEDLINE-97454279; PubMed-9310354; Richards A.J., Luccarini C., Pope F.M.; "The structural organisation of LAMA4, the gene encoding laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMININ ALPHA-4 CHAIN.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
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InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
Pfam; PF00053; laminin_EGF; 3.
Pfam; PF00054; laminin_G; 3.
                                                                                                    3ur. J. Biochem. 248:15-23(1997)
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EMBL, X91171; CAA62596.1; --
EMBL, X7639, CAA74636.1; --
EMBL, X76399, CAA54258.1; --
EMBL, Z99289; CAB16553.1; --
HSSP; P02468; 1KLO.
MIM; 600133; --
                                                                                                                                                SEQUENCE OF 236-1816 FROM N.A.
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64 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDGSGYCVHCQRNTTGEHCEKCLDGYIGDSI 122
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DOMAIN II AND I.
LAMININ G-LIKE 1.
LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 3.
LAMININ G-LIKE 5.
LAMININ G-LIKE 5.
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BY SIMILARITY.
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D -> A (IN REF. 4).
Y -> H (IN REF. 1).
T -> P (IN REF. 1).
SGR -> GGP (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04E9AF379A0F4A4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (PROBABLE)
INTERCHAIN (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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L -> F (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.4%; Score 58; DB ilarity 21.0%; Pred. No. 27; Conservative 13; Mismatches
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Best Local Similarity
Matches 13; Conserva
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3

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5 CSONEYFDSLLHACIPCQLRCSS-NTPPLTCQRYC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 708 AA
                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                Query Match 20.2%; Score 57.5; Best Local Similarity 34.3%; Pred. No. 29; Matches 12; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB032966; BAA86454.1; -.
InterPro; IPR001440; TPR.
Infam; PF00515; TPR; 7.
SMART; SM00028; TPR; 3.
Hypothetical protein; Repeat; TPR repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.6.4.00
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TPR
TPR
TPR
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                                                                                      109
130
203
443
481
928
1061
   1346
1393
1444
1532
1680
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2297
381
415
449
628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                              1061
1182
1275
1278
1440
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264
347
383
416
595
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                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                         CARBOHYD
                                            FRANSMEM
                                                                          CARBOHYD
                                                                                                       CARBOHYD
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REPEAT
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                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                     respective precursors.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY: FURIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_EER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane;
Multigene family; Zymogen; Repeat...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
SIMILARITY)
                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILA
(BY SIMILA
(BY SIMILA
, CYS-RICH.
                              01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Furin-like procease 2 precursor (EC 3.4.21.75) (Furin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FURIN-LIKE PROTEASE 2.
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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FlyBase; FBgn0004598; Fur2.
InterPro: IPR000561; EGF-like.
InterPro: IPR0005174; Furin-like.
InterPro: IPR002084; P_domain.
InterPro: IPR00209; Peptidase_S8.
Pfam: PF00757; Furin-like; 1.
Pfam; PF00483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF00082; Peptidase_S8; 1.
Promom: PD000717; P_domain; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 x ... 55. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ... 7. ..
                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-92381036; PubMed=1512259;
                Created)
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1680
418
457
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1007
1057
            01-APR-1993 (Rel. 25, 01-APR-1993 (Rel. 25, 15-JUL-1998 (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638
962
1008
1008
1105
11154
1206
                                                                                                                                                 NCBI_TaxID=7227
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of CDNA clones selected by the GeneMark analysis from size-fractionated CDNA libraries from human brain.";
DNA Res. 6:329-336(1999)
-i- SIMILARITY: CONTAINS 8 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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MEDLINE-20039618; PubMed-10574461;
Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                  (GLCNAC. . . )
                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                               0A99CE8770A8E293
                                               N-LINKED (GLCNAC.
                                                                                                                                    (GLCNAC.
                                                                                                          (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA1140 (Fragment).
KIAA1140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1199 CSESEFYSQVEGQCRPCHASCGSCNGPADTSCTSC 1233
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ä

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                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                      STRAIN=972;
Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 1; Length 708;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAGQCSQNEYFDSLL--HACIPCQLRCSSNTPPLTCQRYCNASVTNSVK 47
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Indels
                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 81.8 kba protein C2G11.05C in chromosome I. SPACZG11.05C.
TPR 7.
TPR 8.
8B93440B522CFC1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E13EB4C4AE085671 CRC64;
                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces. NCBI_FaxID=4896;
                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                          277 CGKSAYAVSLLRECV -- KLRPSDPTVPLMAAKVCIGSL 312
                                                                                        5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028983;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                              701 AA.
                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.9%; Score 56.5; I 28.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                              PRT;
 662 TP
696 TP
79140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81769 MW;
                                                20.1%;
llarity 36.8%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 254354; CAA91170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004328; BR01.
Pfam; PF03097; BR01; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 701 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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630
663
708 AA;
                                                            Similarity
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                            YAB5_SCHPO
Q09807;
                  SEQUENCE
                                                  Query Match
                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZAN_PIG
  REPEAT
                                                                                                                                        RESULT 12
YAB5_SCHPO
          REPEAT
                                                            Best Loca
Matches
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                                                                                                                                                                                                                   J. Biol. Chem. 270:26025-26028(1995).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TG THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                          EXCLUSIVELY ON THE
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(MUCIN-LIKE DOMAIN).
VWFD 1 (PARTIAL).
VWFD 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 COMA. PELLUCIDA.

2.ONA PELLUCIDA.

-!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPHODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OF PROMOTING ADHESION TO THE OVIDUCITAL ISTHMUS.
-!- DOMAIN: THE WAPD DOMAINS 2 AND 3 MAY MEDIATE CYPALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-!- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAING ARE MISSING FROM THE ZONADHERIM THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
                                                                                                                                                                                                                                                                                                                      -!- SUBULIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON TYPETCAL FREGION OF THE SPERM HEAD (BY SIMILARITY).
-!- TISSUE SPECIFICITY: IL TESTIS, PRIMARILY IN HARLOID SPERMATIDS.
NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
-!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
                                                                                                        Hardy D.M., Garbers D.L.;
A sperm membrane protein that binds in a species-specific manner the egg extracellular matrix is homologous to von Willebrand factor.";
920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; |1624-1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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-!- SIMILARITY: CONTAINS 4.5 VWFD DOMAINS.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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                            1658-1667; 1777-1795 AND 1914-1921.
STRAIN-MEISHAN; TISSUE-Testis;
MEDLINE-96064658; PubMed-7592795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAM 1.
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InterPro; IPR0009561; EGF-like.
InterPro; IPR000999; MAM.
InterPro; IPR002919; TIL.
InterPro; IPR003328; TILa.
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EGF_2; 4.
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Pfam; PF00094; vwd; 4.
SMART; SM0181; EGF; 1.
SMART; SM00137; Mam; 1.
SMART; SM00214; VWC; 2.
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PROSITE; PS50060; MAM_2;
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Pfam; PF01826; TIL; 5.
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PROSITE; PS01186;
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PROCESSING
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN—SPRAGUE-DAWLEY, TISSUE-Mammary gland;
MEDLINE-95094788; PubMed-8001549;
Guenette R.S., Mooibroek M., Wong K., Wong P., Tenniswood M.;
Cathepsin B, a cysteine protease implicated in metastatic
progression, is also expressed during regression of the rat prostate and mammary glands..;
Eur. J. Blochem. 226:311-321(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 69-339 FROM N.A.
MEDLINE-85190489; PubMed-2986112;
San Segundo B., Chan S.J., Steiner D.F.;
"Identification of cDNA clones encoding a precursor of rat liver cathepsin B.";
                                                                                                                                                                                            (POTENTIAL).
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-> Y (IN REF. 1; AA SEQUENCE).
-> Y (IN REF. 1; AA SEQUENCE).
-> K (IN REF. 1; AA SEQUENCE).
-> A13B690375A6548C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 1; Length 2476;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.JUL-1986 (Rel. 01, Created)
1-JUL-19996 (Rel. 34, Last sequence update)
01.ROV-1997 (Rel. 35, Last annotation update)
Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (RSG-2).
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                                 BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC...)
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TISSUE-Liver;
MEDLINE-83221657; PubMed-6574504;
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31.68;
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Best Local Similarity 31.6
Matches 12; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T. "Structure of rat procathepsin B: model for inhibition of cysteine protease activity by the proregion.";

Structure 4:406-416(1996).

C. '- FUNCTION: THIOL PROPESS WHICH IS BELIEVED TO PARTICIPATE IN INTRACELLULAR DEGRADATION AND TURNOVER OF PROTEINS. HAS ALSO BEEN IMPLICATED IN TUMOR INVASION AND METASTASIS.

C. CATALYTIC ACTIVITY: HYDROLYSES PROTEINS, WITH A SPECIFICITY RESEMBLING THAT OF PAPAIN.

C. SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN CROSS-LINKED BY A DISCURLEDE BOND.

C. SUBCELLULAR LOCATION: LYSOSOMAL.

C. SUBCELLULAR LOCATION: LYSOSOMAL.

C. SUBLIBRITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-95197558; PubMed-7890671;
Jia Z., Hasnain S., Hirama T., Lee X., Mort J.S., To R., Huber C.P.,
"Crystal structures of recombinant rat cathepsin B and a cathepsin B-
inhibitor complex. Implications for structure-based inhibitor
design.";
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PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00649; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
Hydrolase; Thiol protease; Lysosome; Glycoprotein; Zymogen; Slgnal;
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                                                                                                                                                                                                                                                                     Rowan A.D., Mason P., Mach L., Mort J.S.; "Rat procathepsin B. Proteolytic processing to the mature form in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 18-339.
MEDLINE-96311276; PubMed-8740363;
Cygler M., Sivaraman J., Grochulski P., Coulombe R., Storer A.C.,
                                           and
Takio K., Towatari T., Katunuma N., Teller D.C., Titani K.; "Homology of amino acid sequences of rat liver cathepsins B with that of papain.";
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ACTIVATION PEPTIDE.
CATHEPSIN B.
CATHEPSIN B LIGHT CHAIN.
CATHEPSIN B HEAVY CHAIN.
                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 80:3666-3670(1983).
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InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 267:15993-15999(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 270:5527-5533(1995).
                                                                                                                                                                                                                                 MEDLINE-92348471; PubMed-1639824;
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PDB; ICPJ; O7-DEC-95.
PDB; IMIR; 11-JAN-97.
PDB; ICTE; 31-JUL-95.
PDB; ITHE; 10-MAR-96.
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SIGNAL
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TISSUE-Brain;

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And Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Beloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
A Deloukas P., Matthews G. Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Balley J., Barlow K.F., Blakey S.E., Berid C.M., Brown A.J.,
Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA RAY M.P., Kimberley A.M., King A., Kinghts A., Laird G.K., Lawlor S.,
Lehvaslaino M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA MINE S., Mistry D., Moconachie L.J., McLay R., McMurray A.A.,
RAISH V.L., Martin S.L., McConnachie L.J., McCapa M., Rams R.,
Rhillimcre B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Ryamn M., Sycamore M.J., Soderlund C., Steward C.A., Sulston J.E.,
Swann M., Sycamore N., Taylor R., Tee L., Williams L., Williams S.A.,
Ryitiehead S.L., Whittaker P., Willey D.L., Williams L., Williams L., Willing D.L., Willing D.L., Willing D.R.,
Ryam R., Ross R., Willey D.L., Williey D.L., Willings D.R.,
Ryamining L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Ryamore J. T.
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                     DB 1; Length 339;
                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 NSHIGCLPYTIPPCEHHVNGSRPPCTGEGDTPKCNKMCEAGYSTSYK 220
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                                                                                                                                                                                                                                   925E2E58C2B03CDA CRC64;
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V -> A.
W -> G (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                  score 55.5; DB; Pred. No. 11; 7; Mismatches
SIMILARITY.
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SIMILARITY.
SIMILARITY.
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SEQUENCE OF 2051-3695 FROM N.A.
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                                                                                                                                                                                                                                   37470 MW;
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Best Local Similarity
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LMA5_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are to restrictions on its use by non-profit institutions as long as its content is in no way
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R InterPro; IPP0019191; Laminin_EGF.

R InterPro; IPP0019191; Laminin_G.

R Pfam; PF00053; laminin_G.

R Pfam; PF00054; laminin_G.

R Pfam; PF00054; laminin_G.

R Pfam; PF00052; Lamg; 2.

R SMART; SM00282; Lamg; 2.

R PROSITE; PS00186; EGF_L: 19.

R PROSITE; PS01186; EGF_L: 19.

R PROSITE; PS01186; EGF_L: 19.

R PROSITE; PS01284; LAMININ_TYPE_EGF; 16.

R PROSITE; PS0025; LAM G_DOMAIN; 5.

R ROSITE; PS60025; LAM G_DOMAIN; 5.

R ROSITE; PS60025; Lamg; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: DOMAIN G IS GLOBULAR AND IS PART OF THE MAJOR CELL-BINDING SITE LOCATED IN THE LONG ARM OF THE LAMININ HETEROTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION AND ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-:- SUBUNIT: LAMININ-15 COMPLEX IS AN HETEROTRIMER COMPOSED OF THREE CHAINS (ALPHA-5)FETA-2/GAMMA-3) WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG AND THREE SHORT ARMS WITH GLOBULES AT EACH END

-:- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

-:- TISSUE SPECIFICITY: EXPRESSED IN HEART, LUNG, KIDNEY, SKELETAL MUSCUE, PANDREASS, RETINA AND PLACENTA. LITTLE OR NO EXPRESSION IN
                                                                                                                                                                                                                                                                                                                                                                                                         MEDILNE=20422761; PubMed=10964957; Libby R.T., Champliaud M.-F., Claudepierre T., Xu Y., Gibbons B.P., Koch M., Burgeson R.E., Hunter D.D., Brunken W.J.; Laminin expression in adult and developing retinae: evidence of two
                                                                      "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                          Albrechtsen R.,
                                                                                                                                                                                                                                                                                                "Tissue-specific expression of the human laminin alpha5-chain, and mapping of the gene to human chromosome 20q13.2-13,3 and to distal mouse chromosome 2 near the locus for the ragged (ka) mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAÎN (DOMAIN VI).
-:- SIMILARITY: CONTAINS 21.5 LAMININ EGE-LIKE DOMÂINS.
-:- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
-:- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                           Kotani
                                                                                                                                                                                                            TISSUE-Placenta;
Bubber 1271224;
Durkin M.E., Loechel F., Mattel M.-G., Gilpin B.J.,
Wewer U.M.;
               MEDLINE=98290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL354836; CAC22309.1; ALT_SEQ.
EMBL; AB067494; BAB67800.1; -.
EMBL; AB011105; BAA25459.1; -.
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                                                                                                                                                                                            SEQUENCE OF 2743-3695 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel CNS laminins.";
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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562222 seqs, 172994929 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database :																

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O88472 mus musculu	Q22378 caenorhabdi	088714 mus musculu	Q9dbz3 mus musculu	Q9et35 mus musculu	017496 ascaris suu	Q9bi07 entamoeba h	Q99nd0 mus musculu	014836 homo sapien	077419 ascaris suu	O18118 caenorhabdi	Q9gq45 giardia lam	Q26489 spodoptera	Q9d8d0 mus musculu	Q9d351 mus musculu	Q17969 caenorhabdi
SUMMARIES	ID	038472	022378	088714	Q9DBZ3	Q9ET35	017496	Q93107	00N660	014836	077419	018118	09G045	026489	Q9D8D0	Q9D351	017969
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17 62.5 22.0 1513 5 017970 18 61.5 21.7 353 5 099W81 20 61.5 21.7 483 5 022423 21 60.5 21.3 1574 11 089381 22 60.5 21.3 1574 11 089381 23 60 21.1 250 12 099W27 24 60 21.1 250 12 099W27 25 60 21.1 250 12 099W27 26 60 21.1 369 5 099W27 27 59.5 21.0 86 13 099W07 28 59 20.8 263 15 099W08 31 59 20.8 263 15 099W08 32 59 20.8 263 15 099W08 33 59 20.8 263 15 099W08 34 59 20.8 263 15 099W08 35 59 20.8 263 15 099W08 36 59 20.8 263 15 099W08 37 59 20.8 263 15 099W08 38 59 20.8 263 15 099W28 39 59 20.8 263 15 099W28 40 59 20.8 263 15 099W28 41 59 20.8 263 15 099W24 42 59 20.8 263 15 099W24 43 59 20.8 263 15 099W24 44 59 20.8 263 15 099W24 45 59 20.8 263 15 099W24 46 59 20.8 263 15 099W24 47 59 20.8 263 15 099W24 48 59 20.8 263 15 099W24 49 59 20.8 263 15 099W27 40 59 20.8 263 15 099W27 41 59 20.8 263 15 099W27	ALIGNMENTS RESULT 1 088472 PRELIMINARY: PRT: 185 AA.	08, Created) 08, Last sequence 17, Last annotati N (TUMOR NECROSIS	DE MEMBER 17). GN THREF17. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae OX NEL_TAXID=10090;	RP SEQUENCE FROM N.A. RC STRAIN-BALB/C; TISSUE-SPLEEN; RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzo RA LeConiat M., Mornon JP., Berger R., Tsapis A.; RT "Murine BCMA: a new member of the Tumor Necrosis Fa RI Superfamily."; RI Superfamily."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ datab	RA SEQUENCE FROM N.A. RC STRAIN=C57BL/6J; TISSUB=COLON; RA MEDINR=210B5660; PubMed=11217851; RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alawa J., Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Batalov S., Zasavant T., Raicchmann W., Gassterland T., Gissi C., King B., Kochiwa H., Reischmann W., Gassterland T., Gissi C., King B., Kochiwa H., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T. Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

⁽Without dilgnments) 98.052 Million cell updates/sec

US-09-854-864-6 284 1 MAGQCSQNEYFDSLLHACIP......LTCQRYCNASVTNSVKGTNA Title: Perfect score: Sequence:

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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sator K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K. H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                          "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AR061505, AAC23799.1;
EMBL; AR020247; BAB23038.1;
MGD; MGI:1343050; Thfrsf17.
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                                                                                                                                                                 65.5%; Score 186; DB 11; Length 185; 71.4%; Pred. No. 2.8e-19; tive 4; Mismatches 8; Indels 7
                                                                                                                                                                                                                                  1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.; "Direct Submission."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL: u39644, AAA80360.2; HSSP; P10969; 1MGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. elegans cosmid T10E10.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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966 AA; 102460 MW; B565A3CDD25216D9 CRC64;
                                                                                                                            20442 MW; 8806352B4FD26A8E CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 102.5 KDA PROTEIN.
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PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002899; EB.
InterPro; IPR002099; EB.
InterPro; IPR00371; Snake_toxin.
Pfam; PF01607; Chitin_bind_2; 2.
SMART; SM00289; wpl. 1.
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                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed=9851916;
                                                                                                                                                                             Best Local Similarity 71.4 Matches 35; Conservative
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                             185 AA;
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Geisel C.;
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                                                   Hayashizaki Y.;
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3;

Gaps

2,

26.2%; Score 74.5; DB 5; Length 966; 36.7%; Pred. No. 0.031; tive 11; Mismatches 15; Indels

Query Match Best Local Similarity 36.78 Matches 18; Conservative

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DECENTAL CSTREAL OF THE SUB-LUNG;
MEDLINE-21085660; PubMed=11217851;
MEDLINE-21085660; PubMed=11217851;
MEDLINE-21085660; PubMed=11217851;
Avanal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Salto T., Okazaki Y., Gojobori T., Bonoo H., Kasukawa T., Salto R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Waqner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rio M.C.; "Identification of interactions between trefoil peptides and members of the mucin protein family using the yeast two-hybrid system."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AJ000752; CAA09343.1;
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                     215 QCSQSTVFNSDLNVCVPLAIQNSCDSSTQQPVCS--C-SQVSSSCPGTS 260
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4 QCSQNEYFDSLLHACIPCQLR -- CSSNTPPLTCQRYCNASVTNSVKGTN
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                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GASTRIC MUCIN-LIKE PROTEIN (FRAGMENT).
GASTRIC MUCIN-LIKE.
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Last annotation update)
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48.3%; Pred. No. 0.03;
tive 1; Mismatches 7;
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
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InterPro; IPR002919; TIL.
InterPro; IPR001846; Vwd.
Pfam; PF01826; TIL; 1.
Pfam; PF00094; vwd; 1.
SMART; SM00216; VWD; 1.
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Best Local Similarity 48.3'
                                                                                                                                                             PRELIMINARY;
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SEQUENCE
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us-09-854-864-6.rspt

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MEDLINE=99339391; PubMed=10413046;
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                                                                                                                                                                                                                                                      Receptor.
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MEDLINE=21177254; PubMed=10881172;
Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in
Blaké J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang X.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                          Hayashizaki Y.;
Hayashizaki Y.;
Hayashizaki Y.;
Hayashizaki Y.;
Hunctional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).

EMBL; AK004668; BAB23457.1;
MGD; MGI:1889411; Infrsf13b.

SEQUENCE 249 AA; 26981 MW; 6F4290D719FEA037 CRC64;
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                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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EMBL; AF257673; AAGO0081.1; -.

MGD; MGI:1889411; Tnfrsf13b.

SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;
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Last annotation update)
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Pred. No. 0.021;
----hes 13;
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                                                                                                                                                                                                                                                                                                                                                         Query Match 25.2
Best Local Similarity 35.3
Matches 12; Conservative
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NCBL_TaxID=6253;
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Q9ET35;
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"Alternative-splicing of serotonin receptor isoforms in the pharynx
and muscle of the parasition nematode, Ascaris suum.";
Mol. Biochem. Parasitol. 101:95-106(1999).
BMBL, AF005486; AAC78396.1;
Interpro. PR00001; 7tm.1; 1.
Pfam; PF00001; 7tm.1; 1.
PRONSITE; PS000237; GPRCHODOPSN.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_1; UNKNOMN_1.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         20;
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0
                                                                                                                                                                                                                            Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 718;
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                                                                                                                                                                                                                                                           ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSWKG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718 AA; 80231 MW; FFF6362A49F2827A CR¢64;
                                                                                                                                                                             60140 MW; 4D795D1C249D55F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update
PUTATIVE CYSTEINE SURRACE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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Pred. No. 0.073;
6; Mismatches 2
                                                                                                                                                                                                                          25.0%; Score 71; DB 5; 24.2%; Pred. No. 0.053; iive 14; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       718 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 5374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Entamoeba histolytica.
Eukaryota, Entamoebidae, Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%; 27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.0
Best Local Similarity 27.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                             532 AA;
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZAN (ZONADHESIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5759;
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Gaps
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MEDLINE-90297373: PubMed-9635450;

Lu C.C., Mayyen T., Morris S., Hill D., Sakanari J.A.;

Lu C.C., Mayyen T., Morris S., Hill D., Sakanari J.A.;

Lu S., Morris S., Hill D., Sakanari J.A.;

Lu C.C., Mayyen T., Morris S., Hill D., Sakanari J.A.;

Lu Anisakis Simplex: mutational bursts in the reactive site centers of serine protease inhibitors from an ascarid nematode.";

Exp. Parasitol. 89:257-261(1998).

Exp. Parasitol. 89:257-261(1998).

EMBL.

InterPro; IPR002919; TIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
    "NF-AT activation induced by a CAML-interacting member of the tumor
                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                  4; Length 293;
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Pred. No. 0.022;
8; Mismatches 18; Indels
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 QCSQNEYFDSLLHACIPCQLRCS--SNTP-PLTCQR-YCNASVTNSVKGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
Wilkinson J.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                    necrosis factor receptor superfamily.";
Science 278:138-141(1997).
EMBL, AF023614; AAC51790.1; -
InterPro: IPROSTS 178R_C.
PROSTIE; PS00652; TWRR_NGFR_1; UNKNOWN_1.
SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154CE25A375E0B2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHYMOTRYPSIN/ELASTASE INHIBITOR-1 (FRAGMENT).
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Last sequence update)
Last annotation update)
                                                                                                                                                                            Score 67.5; DB 4; I
Pred, No. 0.093;
                                                                                                                                                                                                                                                                                                             | : :|:| || |: |: |: |: |: |34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
                                                                                                                                                                                                                                                                                         CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                  23.8%;
30.6%;
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6794 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.6%;
illarity 33.3%;
Conservative
                                                                                                                                                                                                                                                Conservative
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NON_TER 1 1
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Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T23F1.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998
01-JAN-1998
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SEQUENCE
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018118
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                                                                                                                                                   Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P., Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.; "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=129/SV;
Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
"Genomic Basis of Inter- and Intra-species Variation in Zonadhesin
Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                          90D2D8CFE5DE24EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSMEMBRANE ACTIVATOR AND CAML INTERACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%; Score 69.5; DB 11;
36.8%; Pred. No. 0.98;
Live 5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3297 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 18.
EGF-1: PS50060; MAM_2; 3.
EGF-1: de domain; Glycoprotein.
SEQUENCE 5374 AA; S79536 MM; 9C
                                                                                                                              MEDLINE-21138439; PubMed-11239002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1];
SEQUENCE FROM N.A.
MEDLINE-97458245; PubMed-9311921;
VON BULOW G.U., Bram R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00001; EGF_like; 1.
SMART; SM00274; FOLN; 21.
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05,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fam, PF00629; MAM; 3.
fam; PF01826; TIL; 25.
fam; PF02345; TILa; 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00094; vwd; 4.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                   SEQUENCE FROM N.A.
                                        NCBI_TaxID=10090;
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InterPro;
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InterPro;
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Spodoptera frugiperda (Fall armyworm)
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SEQUENCE
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                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 AGQCDQGTYADPTTGQCKPCGITDCATCEYNATISQPQCKTCSTSSNKMYKTAADGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                    "A segment of a vsp72-like gene homolog from a type A-I (group 1)
                                                                                                                                                                      .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGQCSQNEYFDSLLHACIPCQL----RCSSN---TPP--LTCQRYCNASVINSVKGT
                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%; Score 65.5; DB 5; Length 548; 33.3%; Pred. No. 0.35; ive 3; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                               Giardia lamblia (Giardia intestinalis).
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
NCBL_TaxID=5741;
                                                                                                                                                                                          5 CSQNEYFDSLLHACIP----CQLRCSSNTPPL---TCQRYCNASVTNSVKGT
                                          Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                             Score 66; DB 5; Length 330;
Pred. No. 0.17;
8; Mismatches 22; Indels
                                                                                                                                                                    22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glardia intestinalis isolate,";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR298802, AA337862.1;
HSSP: POOL362; 2CY3.
INTERPRO; IPRO00345; CytC_heme_bind.
InterPro; IPRO00561; EGF-like.
InterPro; IPRO0174; Furin-like.
SMART; SM00101; EGF, 2.
SMART; SM00001; EGF_like; 1.
SMART; SM00001; EGF_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578FE4FDA0A2CF0E CRC64;
                                                                                                              F043B1A90D3A8FE9 CRC64;
                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VARIANT-SPECIFIC SURFACE PROTEIN M21-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1
                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                         PRT;
        SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                    investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81129; CAB03405.1; -.
InterPro; IPR003341; DUF139.
Pfam; PF02363; DUF139; 7.
SEQUENCE 330 AA; 36605 WW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ot-nov-1996 (Tremblrel. 01, C. 01-NOV-1996 (Tremblrel. 01, Le 01-DEC-2001 (Tremblrel. 19, La ENDOPROTEASE FURIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56557 MW;
                                                                                                                                              23.2%;
28.3%;
                                                                                                                                                                                                                                                                                 09G045;
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548
                                                                                                                                                                                                                                                                                                                                                                                                                       Mansouri M., Ey P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 AA;
                                                                                                                                                      Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-AD-1;
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01-DEC-2001
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NON_TER
SEQUENCE
                                                                                                                                               Query Match
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                                 none;
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Q9GQ45
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Q26489
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Anzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.S., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Fuuro M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ryons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Antone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Eŭkaryota; Metazoa; Arthropoda; Tracel, Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Wakaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                     rom Spodoptera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ndels
                                                                                                                                                                                                                    frugiperda (Sf9) cells.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z6888; CAA93116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
2010006P15RIK PROTEIN (BAFF RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS---
                                                                                                                          SEQUENCE FROM N.A.
TISSUE-SEP9, FALL ARMYWORM OVARY;
Cieplik M., Klenk H.;
"Cloning and functional characterization of FURIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4C3799C7BBC572AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65.5; DB Pred. No. 0.86; B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002884; P. domain. Pfam; PF0148; P; 1. Pfam; PF00082; Peptidase_S8; 1. Prints: PR00723; SUBTILISIN. ProDom; PD000717; P_domain; 1. SWART; SW00761; FU; 10. PROSITE; PS00136; SUBTILASE_ASP; 1. PROSITE; PS00138; SUBTILASE_IS; 1. PROSITE; PS00138; SUBTILASE_IS; 1.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002174; Furin-like.
InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1299 AA; 142020 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.1%;
34.0%;
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Best Local Similarity
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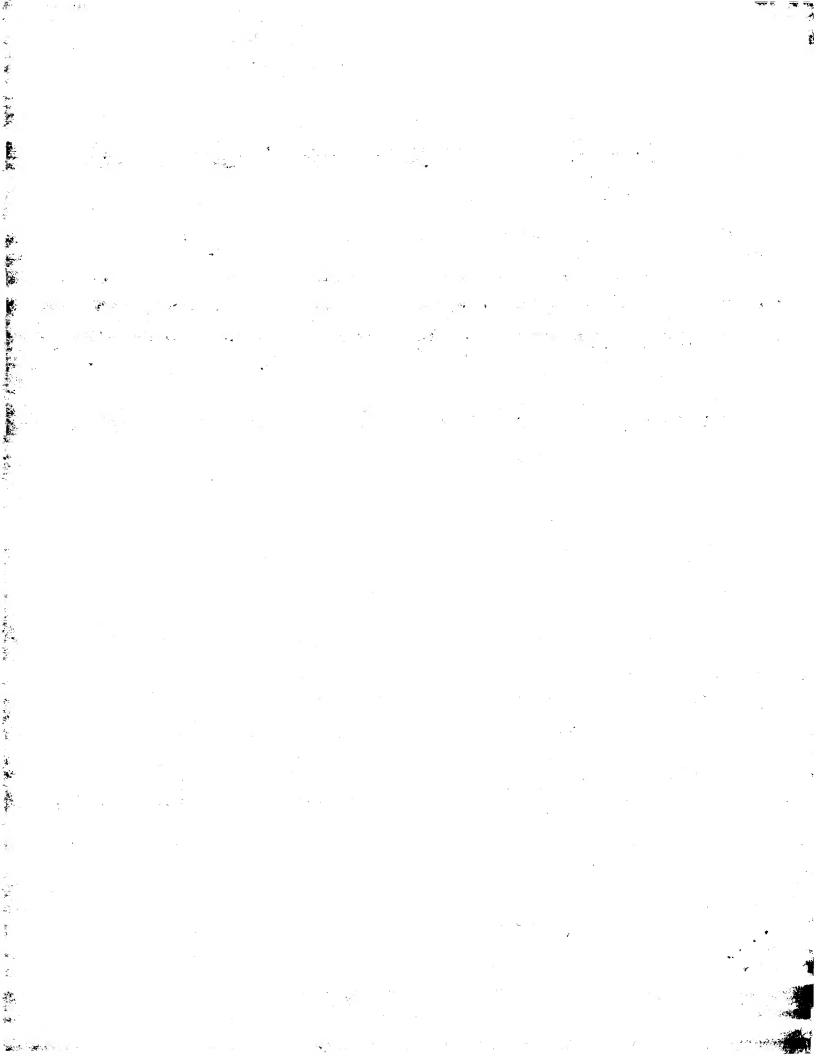
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Frkuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Frkuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Frkuda S., Alizawa K., Izawa M., Nishi K., Kisho H., Kondo H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Mordone P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Storch K.-F., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Masshia M., Washia S., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                  STRAIN-BALB/C;
Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Cachero T.G., Hession C., Schneider P., Slzing I., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
Ambrose C.;
"BAFF-R, a novel TNF receptor that specifically interacts with BAFF.";
Science 0:0-0(2001):
EMBL, AK008142; BAB25490.1; -.
EMBL, AR737847; AR491827.1; -.
MGD; MGI:1919299; 2010006P1SRik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK018361; BAB31177.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 11; Length 175; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-IN VITRO FERTILIZED EGGS; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P08047; 1SP1.
MGD; MGI:1922003; 7420700M05Rik.
INTERFO; IPRO00822; Znf-C2H2.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_ETIGER_C2H2_1; 1.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.2%;
Best Local Similarity 50.0%;
Matches 10; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 QCNQTECFDPLVRNCVSCEL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QCSQNEYFDSLLHACIPCQL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TREMBLrel. 19, 7420700M05RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
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SEQUENCE
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Q9D351
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341 AA; 38094 MW; A332DB7FE231AFFC CRC64;

SEQUENCE

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on:

June 25, 2002, 16:11:20 ; Search time 88.08 Seconds (without alignments) 64.314 Million cell updates/sec

US-09-854-864-6 284

Title: Perfect score: Sequence:

1 MAGQCSQNEYFDSLLHACIP.....LTCQRYCNASVTNSVKGTNA

51

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Searched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_032802;

| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA1991.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA1993.DAT:*

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* /SIDS1/gcgdata/geneseg/genesegp-embl/AA1995.DAT:*/SIDS1/gcgdata/geneseg/genesegp-embl/AA1996.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Amino acid sequence	A human BCMA prote	Human BCMA proteir	Human B celî matur	Human BAFF recepto	Human B cell matur	Human BCMA-Immunoc	Mouse IqG siqnal/	Human BAFF recepto	Amino acid sequenc	Murine B cell matu
	ID		AAY94001	AAE09241	AAE00506	AAB60698	AAY71979	AAE00507	AAB60699	AAB60700	AAB08844	AAY71980
	B :	21	21	22	22	22	22	22	22	22	21	22
	Length	184	184	184	184	184	184	302	302	157	185	185
% Query	re Match Length DB I	100.0	100.0	100.0	100.0	100.0	100.0	95.1	95.1	71.0	65.5	65.5
	Score	284	284	284	284	284	284	270	270	201.5	186	186
Result	NO.	1	7	m	4	S	Q	7	80	6	10	11

ine ztnf4, a	Human Lymphocyte s Human TACI splice	Human lymphocyte s	Human neutrokine-a	A transmembrane ac	Human TACI protein		Novel human diagno			æ	Human BR43x2, an i	Drosophila melanog	nin	Mouse laminin 8 po	terin	Drosophila melanog		nin 8	8		nin 8	Drosophila melanog	me1	me]	ď	æ	a		phila me	2	Novel human diagno	Pig p105 zona pell	
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on r	AAE0924		AAB3631	AAY94000	AAE0924	AAY7191	10	AAG6588'	38595	B7155	7.83399	B7154	.B4844	B4844	.04105	ABB63128	B6649	B4844	AAB4844	AAB4844	AAB4844	ABB7151	ABB6049	B6050	ABB63629	AAU3895	ABG22836	9	ABB6329	G2221	ABG01557	W6773	
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21	22	19	21	21	22	22	22	22	22	22	21	22	21	21	22	22	22	21	21	21	21	22	22	22	22	22	22	22	22	22	22	20	
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12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; geptic shock. Ā AAB08843 standard; peptide; 184 Amino acid sequence of human. (first entry) Homo sapiens 02-JAN-2001 AAB08843; AAB08843 RESULT

Location/Qualifiers 57..77 /note= "putative transmembrane domain" 24-FEB-2000; 2000WO-US04925 WO200050633-A1 31-AUG-2000 Key Domain

(GEHO) GEN HOSPITAL CORP. WPI; 2000-558405/51 Seed B, Ting A;

24-FEB-1999;

Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide

N-PSDB; AAA58559

Disclosure; Page 152; 175pp; English

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polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene expression from a promoter. The method the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, approposity, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                                             is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a
                                                                                                               present sequence represents a BCMA (not defined) polypeptide. BCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 284; DB 21; 100.0%; Pred. No. 2.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY94001 standard; Protein; 184 AA.
                                                                               Claim 32; Fig 7A; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 51; Conservative
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The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor.

Taci is a tumour necrosis factor (TACI) receptor. The extracellular commains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting taffa activity. In EVAN receptor-ligand They may also be used for inhibiting taffa activity. In BAM receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The Itafa activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with a stylm aborder in the stage renal failure, captume, bronchitis, emphysema, end stage renal failure, captume, bronchitis, maphysma, light chain neuropathy, and myltiple myelomas, lymphomas, light chain neuropathy and myelomas, and BRA9 production, graft versus host disease, inflammation, insulin dependent cipection, graft versus host disease, inflammation, insulin anemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery constructs, or occlusion, and cholesterol or renal emboli.

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Gaps

54

100.0%; Score 284; DB 21; Length 184; \ 100.0%; Pred. No. 2.7e-26; \ 1.1ve 0; Mismatches 0; Indels 0;

Query Match
Best Local Similarity 100.

184 AA;

Sequence

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Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis;
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1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA
                4 maggcsqneyfdsllhacipcqlrcssntppltcqrycnasvtnsvkgtna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grewal I,
                                                                                                                                         AAE09241 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2000; 2000WO-US32378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0182938.
2000US-0226986.
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi AJ, Dodge KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                               Human BCMA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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22-AUG-2000;
                                                                                                                                                                                                                       19-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                    psoriasis.
                                                                                                                                                                            AAE09241;
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                                                                                                                      AAE09241
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                                                                                                                                                              Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; activity; antibody production; autofineme disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; emptatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammathon; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yee DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gross JA, Xu W, Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JAN-2000; 2000WO-US00396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0226533
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WO200040716-A2.

13-JUL-2000

Homo sapiens

07-JAN-1999;

Pitti

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Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; Launoglobulin production inhibitor; autoimmune disorder; B-cell immunoglobulin production inhibitor; autoimmune disorder; B-cell immunosuppressive disorder; HTV infection; organ transplantation; antiinflammatory; systemic lipus erythematosus; autoimmune haemolytic annemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphoma; gene therapy; cancer; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60698 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BAFF receptor (BAFF-R).
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11-FEB-2000; 2000US-0181684.
18-FEB-2000; 2000US-0183536.
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(APOT-) APOTECH R & D SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                  (APRIL-R) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, mycloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, poorlasis and lupus erythematosus. The present sequence is human
                                                         Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 284; DB 22; Length 184; I Similarity 100.0%; Pred. No. 2.7e-26; 51; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human B cell maturation protein (BCMA).
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                                                                                                                                                                Example 2; Fig 2; 160pp; English.
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2000US-0181807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APOT-) APOTECH R & D SA.
WPI; 2001-541628/60.
N-PSDB; AAD15902.
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N-PSDB; AAD03844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      3CMA protein.
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30-JUN-2000;
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                                                                                                                        antagonists
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associated with undesired cell proliferation such as condition
associated with undesired cell proliferation such as cancer or
carcinoma. The method involves administering a composition comprising
carcinoma. The method involves administering a composition comprising
carcinoma. The method involves administering a composition comprising
carcinoma between APRIL and its cognate receptor(s). This method is
carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
carcinoma e.g. human lung carcinomas whose proliferation is modulated
carcinoma e.g. human lung carcinomas whose proliferation is modulated
by APRIL. It is also useful for treating autoimmune diseases (Grave's
cliseases, systemic lupus erythematosus.SLB; hypepertension, cardiovascular
diseases, renal disorders, B-cell lympho-proliferative disorders,
immunosuppressive diseases, organ transplantation, inflammation and
thuman immunodeficiency virus (HIV), and for treating, suppressing or
altering an immune response involving a signalling pathway between
APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
The present sequence is human APRIL-R also referred
as BORMA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                             The invention relates to a method of treating a mammal for a condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                administering a
undesired cell
                                           proliferation such as cancer or carcinoma, comprises administer composition comprising A Proliferation Inducing Ligand Receptor
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    Treating a mammal for a condition associated with
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100.0%; Pred. No. 2.7e-26;
iive 0; Mismatches 0;
                                                                                                                                                                                                              Claim 3; Fig 3A; 85pp; English.
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WO200068378-A1.
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                                                                                                                                                                                                                                                                                                                           The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of avariety of immune-related disorders. BAFF-R, as a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative consection, and in patients undergoing organ transplantation. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, crave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly between a systemic parent of the propressive gloomerulonephritis, and lymphomas. Nucleic acids encoding
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                                                                                                                                                     Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 184;
  Browning J, Ambrose C, Tschopp J, Schneider P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 maggcsqneyfdsllhacipcqlrcssntppltcqrycnasvtnsvkgtna 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 284; DB 22; 100.0%; Pred. No. 2.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B cell maturation factor (BCMA) protein.
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/label= Extracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents human BAFF-R.
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                                                                                                                                                                                                                                                                                   Claim 20; Fig 1; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 51; Conservative
                                                                          WPI; 2001-202866/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AA;
                                                                                                          N-PSDB; AAF59998
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MacKay F, |
Thompson J;
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Domain
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The present invention relates to Tumour necrosis factor (TNF) and ApoL-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthiitis, systemic lupus erythematosus (SLE), insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, doodpasture's syndrome, pemphigus vulgaris, carbet sheumatic fever, post-streptococcal glomerulonephittis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.

The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is protein. It is the receptor for TALL-1 protein. BCMA gene is protein. It is the receptor for PALL-1 protein mascle, heart, lung, kidney, spleen and lymph nodes but not by brain, muscle, heart, lung, kidney, pancreas, testis and placenta. BCMA mRNA is absent in the pro-Blymphocyte stage but its expression increases with B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCW; Immunosuppressive disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 284; DB 22; 100.0%; Pred. No. 2.7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 37; Page 104-105; 112pp; English.
                                                                                                                                                                                                                                        (NAJE-) NAT JEWISH MEDICAL & RES CENT
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                                                                                                                                       06-MAY-1999;
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16-NOV-2000
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organ transplantation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMA; fusion protein; immunoglobulin G; IgG; Fc region.
                  - Homo sapiens.
- Mus sp.
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N-PSDB; AAD03847.
                                                                                                                                          BIOJ ) BIOGEN INC.
                                                                                             WO200124811-A1
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30-JUN-2000;
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                                                                                                      12-APR-2001
                  Chimeric
Chimeric
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                                    Protein
                                                  Protein
                                                          Region
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carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by ARRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating a mammal for a condition associated with undesized cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation profein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesized cell proliferation such as cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also referred as BCMA or BCM protein, Fc region of human immunoglobulin G (19G) and a signal sequence from murine 19 kappa cDNA.
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                                                                                                           23..302
/label= Mature_human_BCMA_IgG_Fc_fusion_protein
'23..75
                                                                          /label= Signal_peptide
/note= "Derived from murine Ig kappa sequence"
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                                                                                                                                                                                                                                                                                                                                                            "Derived from human 19G Fc region"
                                                                                                                                                                                                                                                                             "Derived from human BCMA protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Cysteine_rich_domain
/note= "Derived from human BCMA"
Location/Qualifiers
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2000US-0181807.
2000US-0215688.
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Gaps

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Indels

95.1%; Score 270; DB 22; 96.0%; Pred. No. 2.2e-24; tive 1; Mismatches 1;

Conservative

Best Local Similarity

Query Match

48;

Matches

Length 302;

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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative cell infection, and in patients undergoing organ transplantation. The BAFF-R conference in faction, and in patients undergoing organ transplantation. The BAFF-R couperessing or altering an immune response involving a signalling pathway between BAFF-R and BAFF-R and BAFF-R and maturation it is useful for treating diseases inhibits B-cell growth and maturation it is useful for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                    Human BAFF-R; BAFF receptor; TNF family; immunoreghlatory agent; immune-related disorder; B-cell growth inhibitor; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                lupus erythematosus;
                                                                                                                                                                                                                                                                            Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
                                                                                                                                                                                                                                                                                                                                                                                                       renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; b-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; IgG FC; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schneider P;
                      27 magqcsqneyfdsllhacipcqlrcssntppltcqrycnasvtnsykgvd 76
1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTN 50
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                                                                                                                                                   A.
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                                                                                                                                                 AAB60699 standard; Protein; 302
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18-FEB-2000; 2000US-0183536.
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                                                                                                                                                                                                                                  22-MAY-2001 (first entry)
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99US-0121485
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                    157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as BCMA) protein, or a BAFF.R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunorequiatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, tusion proteins containing it, and BAFF-R specific antibodies can be used for inhibiting B-cell growth, dendritic
                                                                                                                                                                                                                                                                                                                                   Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; Immune-related disorder: B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; autoduction inhibitor; autoimmune disorder: B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephriits; lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to the use of a BAFF receptor (BAFF-R, also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog
human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-FC, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human BAFF-R and a human IgG Fc sequence.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                 BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
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                                                                                                          Score 270; DB 22;
Pred. No. 2.2e-24;
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                                                                                                                                  Mismatches
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                                                                                                          95.1%;
96.0%;
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18-FEB-2000; 2000US-0183536.
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                                                                                                                                   48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-202866/20.
N-PSDB; AAF60000.
                                                                                                          Query Match
Best Local Similarity
                                                                        302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                AAB60700;
                                                                         Sequence
                                                                                                                                                                                                                                                                                                                 Human
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cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune heamolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a human BAFF-R protein sequence as encoder by plasmid PJST535. However, this BAFF-R protein sequence is 27 amino acids shorter than that given in AAB60698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 157;
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/note= "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.0%; Score 201.5; DB 2
82.4%; Pred. No. 1.7e-16;
ive 0; Mismatches 0
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           activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple solenosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation; post-streptococcal glomerulonephritis; polyarteritis nodosa.
used to identify compounds which modulate BCMA activity (and thus NF-kB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Tumour necrosis factor (TNF) and ApoL-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                          Score 186; DB 21; Length 185;
Pred. No. 1.4e-14;
4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine B cell maturation factor (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 107-108; 112pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY71980 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                            65.5%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                               35; Conservative
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                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                      185 AA;
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                                                                                                                                                                                                                                                designing
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                                                                                                                                                                                                                                                                                    Sequence
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Best Local 3
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invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, contoinmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, cost-streptococcal glomerulonephritis, or polyarterfitis nodosa.

The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.

The present sequence is a murine B cell maturation factor (BCMA).

BCMA is the receptor for TALL-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TMF; zinf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis, multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vascullitis; nephritis; renal neoplasm; multiple myelonephritis; vascullitis; nephritis; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; maemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
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Pred. No. 1.4e-14;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A murine ztnf4, a tumour necrosis factor ligand.
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                                                                                                                                                                                                                                                                                                                                                                            65.5%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                     185 AA;
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Best Local Simi
Matches 35;
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                                                                                                                                                                                                                                                                                                                       Sequence
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              The present sequence represents murine ztnf4, a tumour necrosis factor ligand. The extracellular domains of BR43x2 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or ECWA (a related B cell protein) contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. They may also be used for inhibiting ztnf4 activity. They may also be used for inhibiting at activity. They may also be used for inhibiting BR43x2, TACI or BCWA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with a autoimmune disease selected from systemic lupus erythematosus, myasthenia autoimmune disease selected from systemic lupus erythematosus, myasthenia carvis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, vasculitis, nephritis, pyelonephritis, renal coplasms, multiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft calabetes mellitus, crohn's disease, inflammation, insulin dependent diabetes mellitus, crohn's disease, joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or artagonists can an euse used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium signal modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B-cell; B lymphocyte; liffection; cancer; rheumatold arthritis; autoimmune disease; glomerulonephritis; immunosuppressive; graft versus host disease; transplant rejection; therapy; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lymphocyte surface receptor extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.5; DB 21;
Pred. No. 0.97;
8; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 cpkdqywdssrkscvscaltcsqrs-qrtctdfc 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                        25.2%;
35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.2%
Best Local Similarity 35.3%
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-506346/43.
                                                                                                                                                                                                                                                                                                                                                                                      249 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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This is the amino acid sequence of the N-terminal, i.e. the extracellular, domain of novel human transmembrane activator and caxtracellular, domain of novel human transmembrane activator and caxtracellular, domain of protein (see AAM75783). TACI is a lymphocyte receptor protein that is involved in the calcium activation pathway. It is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. The extracellular domain of TACI functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the C-terminal portion (see AAM75784) of TACI to the N-terminal domain of CAMI. A recombinant form of the extracellular portion of TACI acts as a dominant-negative or locking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used to a candidate molecule is determined by detecting cellular cativation of the AP-1, CAMP or NF-KB pathway, of NR-AT transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim KJ, Marsters SA, Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67.5; DB Pred. No. 1.9; 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09244 standard; Protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TACI splice variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 6; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.8%;
30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2000; 2000WO-US32378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-2000; 2000US-0182938.
22-AUG-2000; 2000US-0226986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.8
Best Local Similarity 30.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ, Dodge KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-541628/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200160397-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE09244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yan M;
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            antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TWR receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL and TALL-1 with TACI or Block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, mysoloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple solon and proclass and lupus erythematosus. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACI; transmembrane activator and CAML-interactor;
calcium signal-modulating cyclophilin ligand; human;
lymphocyte surface receptor; human; B-call; B lymphocyte;
infection; cancer; rheumatoid arthritis; autoimmune disease;
glomerulonephritis; immunosuppressive; graft versus host disease;
 invention relates to methods of using one or more agonists or
                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and
                                                                                                                                                                                                                                          Length 265;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                         Score 67.5; DB 22;
Pred. No. 3.1;
                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..166
/label= Extracellular_domain
/note= "Claim 8"
167..186
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                      5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187..294
/label= Cytoplasmic_domain
/note= "Claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "TNFR_NGFR motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lymphocyte surface receptor TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            AAW75783 standard; Protein; 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplant rejection; therapy
                                                                                                                                                                 TACI splice variant protein.
                                                                                                                                                                                                                                          23.8%; 30.6%;
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                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bram RJ, Von Bulow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-506346/43.
N-PSDB; AAV57328.
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Matches 11; Conserv
                                                                                                                                                                                               265 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-1998;
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                                                                                                                                                                                                                                            Query Match
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                                                                                                                   activator and CAMA-interactor (TACI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TACI is normally present in E-lymphocytes, and to a much lesses extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. TACI CDNA (seev57328) was isolated from a B-lymphocyte converging a yeast two-hyprid assay. Also claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments of TACI, recombinant DNA constructs, unicellular hosts, and antibodies to TACI protein. Methods are claimed for identifying a claimed for IACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes without affecting mature T lymphocytes. TACI can be activated to increase immune system activity, e.g. for treating infections or cancers. It can be blocked to provide immunosuppression, e.g. for treating autoinmune and inflammatory conditions such as immune complex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s, experimental toid arthritis,
inflammatory conditions, transplant rejection or graft-versus-host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer or
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                                                                                                      This is the amino acid sequence of novel human transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               induced vasculitis, glomerulonephritis, haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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Pred. No. 3.5;
                                                          89pp; English.
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30.6%;
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Best Local Similarity 30.6
Matches 11; Conservative
                                                             Fig 2a;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-290-333-6
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US-08-299-811-4
US-08-99-811-4
US-08-510-133A-3
US-08-510-133A-3
US-08-599-811-2
US-09-042-105-2
US-09-042-105-18
US-08-510-131A-3
US-08-510-131A-3
US-08-510-131A-3
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US-08-465-380-4
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Sequence 40, Appl Sequence 33, Appl Sequence 40, Appli Sequence 36, Appli	THE SAME AND METHODS OF USE	*	Lepgth 166;
28 53.5 18.8 77 2 US-08-461-965-40 53.5 18.8 77 2 US-08-326-110A-33 31 53.5 18.8 77 2 US-08-326-110A-33 32 53.5 18.8 77 2 US-08-634-641-4 32 53.5 18.8 77 3 US-09-249-471-40 33 53.5 18.8 77 3 US-09-249-471-40 35 53.5 18.8 77 3 US-09-249-472-4 35 53.5 18.8 77 3 US-09-249-472-4 37 53.5 18.8 77 3 US-09-249-472-4 37 53.5 18.8 77 3 US-09-249-451-40 38 53.5 18.8 77 3 US-09-249-461-4 41 53.5 18.8 81 2 US-08-489-478-36	RESULT 1 US-08-810-572A-6 Sequence 6, Application US/08810572A Sequence 1, Sequence 6, Application US/08810572A Sequence 6, Application US/08810572A Septent No. 5969102 GENERAL INFORMATION: APPLICANT: Von Bullow, Gotz TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR TITLE OF INVENTION: A LAMP. STREET: A LAIL HARROF STREET: A LAIL HARROF STREET: A LI HACKENSACK AVE, CONTINENTAL PLAZA, A LI HACKEN A LI H	CITY: Hackensack STATE: New Jersey COUNTR: OSA ZIP: O7601 ZIP: O7601 COMPUTER READABLE FORM: MEDIUM TYEE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/810,572A FILING DATE: 28 FFB-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: JACKSON E3G, DAVIG A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 26,742 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800 TELEPHONE: 201-343-1684 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHRACTERISTICS: LENGTH: 166 amino acids:	: TYPE: amino acid ; STRANDEDNESS: single ; TOPOLCGY: linear ; MOLECULE TYPE: peptide ; HYPOTHETICAL: NO ; FRAGMENT TYPE: N-terminal ; ORIGINAL SOURCE: ; ORGANISM: Homo sapiens US-08-810-572A-6 Query Match 23.8%; Score 67.5; DB 2; Lance of the control of the c

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AFFILENT TOTAL BOLOW, GOLZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAME, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                     PHOCYTE SURFACE RECEPTOR THAT BINDS NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                          NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                            COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
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Pred. No. 1;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
 APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE
TITLE OF INVENTION: CAML, NUCLEIC
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
ZIP: 07561
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09290333
Patent No. 631622.
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.8%;
ilarity 30.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 201-487-580
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floor
                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                             COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-810-572A-2
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                                                                                                                                                                                                 Jatent No. 6316zzz
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
ADPLICANT: Bram, GOTZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                       Gaps
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                       1;
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                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                      5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
                                                                                      34 CPEEQYWDPLLGTCMSCKTICNHOS-ORTCAAFCRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.8%; Score 67.5; DB Best Local Similarity 30.6%; Pred. No. 0.56; Matches 11; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNA 40
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APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence(2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
                                                                                                                                                                                       Sequence 6, Application US/09290333
Patent No. 6316222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 166 amino acids TYPE: amino acid
Best Local Similarity 30.6%; Promatches 11; Conservative 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                        Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-810-572A-2
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US-09-290-333-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MOSIKAWA, MINORU
APPLICANT: HARADA, NAOKI
TITLE OF INVENTION: GENE ENCODING 19G FC REGION-BINDING
                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENE ENCODING 19G FC REGION TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.5%; Score 55.5; DB 4; 33.3%; Pred. No. 5.9e+02;
                                                                                                                                                                                        Score 56; DB 2; I
Pred. No. 2.3e+02;
8; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WORPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DCOKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               US-08-718-388-9; Sequence 9, Application US/08718388; Patent No. 6271362
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; Patent No. 5932540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INPORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        Query Match 19.7%;
Best Local Similarity 31.6%;
Matches 12; Conservative
                             2476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5405 amino acids
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        SEQUENCE CHARACTERISTICS
                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-718-388-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-999-811-4
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APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
WUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FTLING DATE: 12-Apr-1999
CLASSIFICATION: <URLOWN</td>

ATTORNEY/AGENT INFORMATION:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPA: 201-343-164
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARRATERISTICS:
LENGTH: 293 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67.5; D
Pred. No. 1;
9; Mismatches
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Arnold, White & Durkee P. D. Box 4433 Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N + terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.8
Best Local Similarity 30.6
Matches 11; Conservative
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Texas
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STREET: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-290-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                              Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        Indels
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Pred. No. 43;
2; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                               Db . 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 296
                                                                                                                          DB 2;
                                                                                                                                                                                                                                                     4 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BRIC K. STEFFE
REGISTATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
                                                                                                                          Score 54.5; D
Pred. No. 43;
2; Mismatches
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
                                                                                                                          19.2%;
35.0%;
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Best Local Similarity 35.0%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202)371-2600
(202)371-2540
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                                                                                                                          Query Match 19.2's
Best Local Similarity 35.0'
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-09-042-105-4
   ; ORGANISM: Homo sapiens
US-08-824-996-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-042-105-4
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Patent No. 5935820
GENERAL INFORMATION:
APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
FILE REFERENCE: PF11201
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
GITY: MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/999,811

FILING DATE: HEREWITH

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,550

FILING BAPLICATION DATA:

APPLICATION NUMBER: US 08/465,968

FILING APPLICATION NUMBER: US 08/465,968

ATTORNEY/AGENT INFORMATION:

NAME: MARKOWICZ, KARRN R.

REGISTATION NUMBER: 36,351

REFERENCE/DOCKET NUMBER: 1488.100004

TELERDOMUNICATION INFORMATION:

TELERDOMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 OCGANREFDENTCOCV-CKRTCPRNOPLNPGKCACECTES 296
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19.2%; Score 54.5; DE
Best Local Similarity 35.0%; Pred. No. 43;
Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-999-811-4
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                USA
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LENGTH: 350
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APPLICANT: HU, JING-SHAN

APPLICANT: ROSEN, CRAIG A.

APPLICANT: CAO, LIANG

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR:
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 NEW YORK AVENUE
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SOFTWARE STATEM.
SOFTWARE STATEM.
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: B-MAR-1994
PRIOR APPLICATION NUMBER: US 08/465,968
FILING DATE: O6-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOMICZ, KAREN R.
       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,895
FILING DATE:
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33072
RELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08999811
Patent No. 5932540
                                                                                                                                                                                                                                                                                                                                                        33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-585-895-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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ZIP: 20005
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US-08-999-811-2
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                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 350;
                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/08585895
Patent No. 6245530
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
258 OCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.2%; Score 54.5; C
35.0%; Pred. No. 43;
Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 33: US-08-510-133A-33
                                                                                                                                                                                   APPLICANT: Alitalo, Kari
Joukov, Vladomir
TITLE OF INVENTION: Receptor Ligand
WUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTX: united States of America
ZIP: 66606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                       RESULT 10
US-08-510-133A-33
; Sequence 33, Application US/08510133A
; Patent No. 6221839
; Patent LINPORMATION:
CRNERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 35.0
Matches 14; Conservative
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US-08-585-895-33
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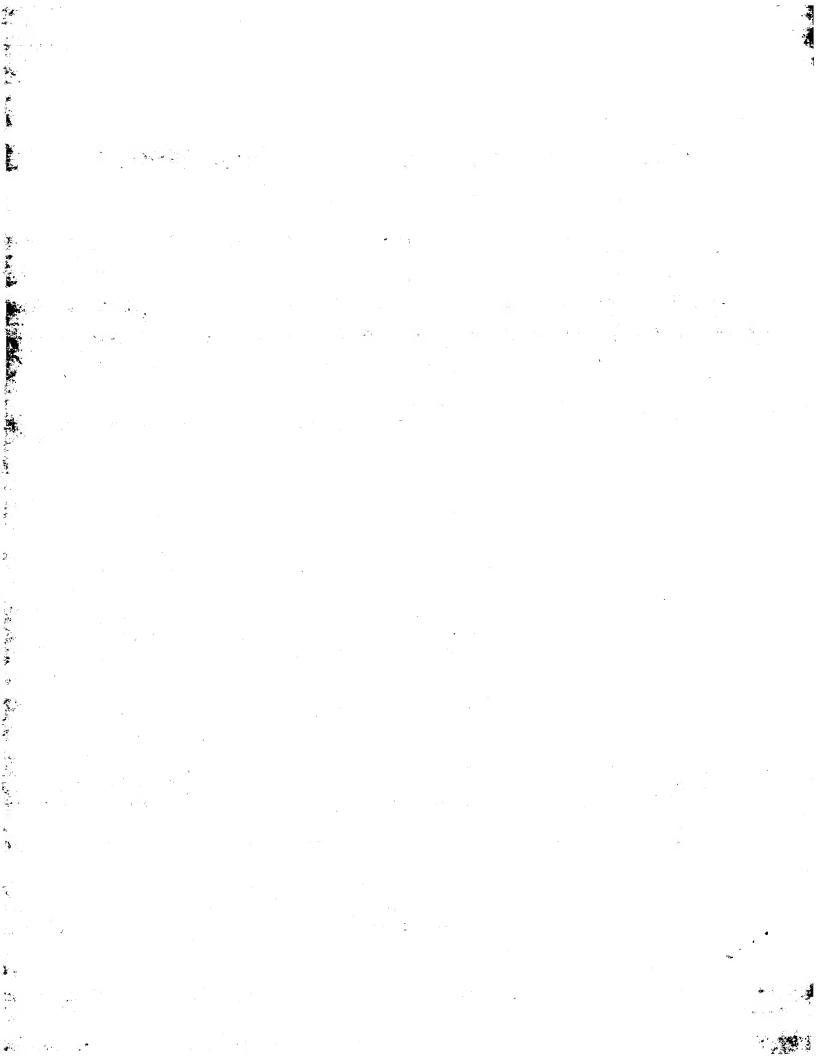
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                                                                                                                                                                                                                                                   APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
TILLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
            21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/042,105 FILING DATE: HEREWITH
                                                                              327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
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                                                  4 OCSONEYFDSLLHACIPCOLRCSSNTP -- PLTCORYCNAS 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.2%; Score 54.5; ilarity 35.0%; Pred. No. 52; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    RESULT 14
US-09-042-105-18
; Sequence 18, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 419 amino acids amino acid
            14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-042-105-18
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Best Local Similarity
Matches 14; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
COUNTRY: US.
ZIP: 20005
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US-08-795-430-8
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            Matches
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                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-042-105-2
Sequence 2, Application US/09042105
Sequence 2, Application US/09042105
Sequence 3, Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/042,105 FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION DATA: PRIOR APPLICATION DATA: CLASSIFICATION NUMBER: US 08/207,550 FILING DATE: #MAR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                     4 OCSONEYFDSLLHACIPCOLRCSSNTP--PLTCQRYCNAS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: STERNE, KESSLER, GOLDSTEIN & FOX 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1488.1000003/EKS
                                                                                                                                                                       Score 54.5; DE
Pred. No. 52;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TOPOLOGY: 11.
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INFORMATION FOR SEQ ID NO: 2:
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35.0%;
                                                                                                                                                                       Query Match 19.2%;
Best Local Similarity 35.0%;
Matches 14; Conservative
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LENGTH: 419 amino acids
TYPE: amino acid
        SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid
                                                                                        ; MOLECULE TYPE: protein US-08-999-811-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-042-105-2
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Best Local Similarity
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2;
Sequence'8, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
ATILE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: G300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: 1010 Sears Tower, 233 South Wacker Drive
CONTRY: United States of America
CONTRY: United States of America
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SUFFICIATION NUMBER: US/08/795,430
FILING DATE: 01-040(-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 14-7EB-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 12-7EB-1996
PRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 12-7AN-1996
PRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 11-040(-1996
PRIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 11-040(-1996
PRIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 11-040(-1996
PROPERIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 11-040(-1996
PROPERIOR APPLICATION NUMBER: 38,153
RECEDENDARIATION NUMBER: 28967/33691
TELECOMMUTCATION NUMBER: 28967/33691
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
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TELEX: 25.3856
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
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Best Local Similarity 35.0%
Matches 14; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-8
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Search completed: June 25, 2002, 16:12:12 Job time: 52 sec



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June 25, 2002, 16:13:20 ; Search time 52.94 Seconds (without alignments) 61.712 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                   OM protein . protein search, using sw model
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US-09-854-864-7 201 1 CSQNEXFDSLLHACIPCQLRCSSNTPPLTCQRYC 34 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

283138

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	B-cell maturation	serine proteinase	zonadhesin - mouse	hypothetical prote		furin (EC 3.4.21.7	chymotrypsin/elast	furin (EC 3.4.21.7	epidermal growth f	zonadhesin - piq				alpha tectorin - m	myosin heavy chain	myosin-IXb simila	finger protein YJL	MEGF6 protein - ra	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	_	protein 2C84.6 [im	hypothetical prote	antimicrobial pept	siah-1B protein -	siah-1A protein -	hypothetical prote	
SUMMARIES	QI	S43486	534583	T42215	T16840	T15577	T43251	807127	A43434	A45558	T34022	T01519	T25169	T23681	T30197	S54307	A59256 ·	S46625	T13954	T22759	S61051	A84544	T23682	T34318	D88550	528291	S57816	S35754	148763	T27827	
	DB 1	7			7			7	7		7	7	7	7	7	7	7	7	7	7			7				7	7	7	0	
	Length	184	1548	5376	1101	756	1299	63	1680	1717	247	986	330	1513	2155	198(202	758	157	2824	118	25	297	54	1474	2844	63	282	282	49	
s Ouerv	Match Length DB	100.0	33.6	32.1	30.3	29.4	28.9	28.6	28.6	28.4	27.9	27.6	27.4	27.4	27.1	26.9	26.9	26.6	26.4	26.4	26.1	25.9	25.9	25.9	25.9	25.9	25.6	25.6	25.6	25.6	
	Score	201	67.5	64.5	61	29	28	57.5	57.5	57	26	55.5	55	55	54.5	54	54	53.5	53	53	52.5	52	52	52	52	52	51.5	51.5	51.5	51.5	
Result	NO.	7	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	

\$34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: (02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: \$34583

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RESULT

30 51.5 25.6 915 2 T21773 31 51.5 25.6 927 2 T21772 33 51.5 25.6 929 2 T19275 34 51 25.4 641 2 E96612 35 51 25.4 641 2 E96675 36 51 25.4 641 2 E96675 37 50.5 25.1 610 1 146001 38 50 24.9 74 2 S08572 40 50 24.9 376 2 C81272 41 50 24.9 376 2 C81272 42 50 24.9 376 2 C81272 44 50 24.9 561 2 T27318 45 50 24.9 561 2 T27318	hypothetical prote hypothetical prote alpha tectorin - c probable transcrip hypothetical prote hypothetical prote CAb-binding protei chymotrypsin/elast ubiquiin / riboso hypothetical prote probable aminotran tumor necrosis fac hypothetical prote probable aminotran tumor necrosis fac hypothetical prote hypothetical prote hypothetical prote
ALIGNMENTS	
RESULT 1 S43486 B-cell maturation factor - human N;Alternate names: BCM protein; BCM c;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 C;Accession: S43486; S31208; S36661	protein #text_change 21-Jul-2000
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; I Nucleic Acids Res. 22, 1147-1154, 1994 A;Title: The BCMA gene, preferentially expressed dur A;Reference number: \$43486; MUID:94218235 A;Accession: \$43486	.; Larsen, C.J.; Tsapis, A. during B lymphoid maturation, is bid
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-184 <laa> A;Cross-references: EMBL:229574; NID:9471244; PIDN:CAA82690.1; PID:947124; R;Labbi, Y; Gras, M.P; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, FNAC 1 1 2867-3004 1902</laa>	:САА82690.1; PID:g471245 3.; Berger, R.; Larsen, С.J.; Tsapi
A.Title: A new gene, BCM, on chromosome 16 is fused A; Reference number: \$31208; MUID:93010984 A; Accession: \$31208	d to the interleukin 2 gene by a t(
A; Molecule type: mRNA A; Residues: 1.184 < CAZ> A; Cross_references: EMBL:214954; NID:g29407; PIDN: A; Accession: S3661 A; Status: preliminary	PIDN:CAA78679.1; PID:929408
A.Residues: 4-184 <la3> A.Residues: 4-184 <la3> A.Cross-references: EMBL:214955 C.Genetics: A.Genetics: A.G. C.G. C.G. A.G. C.G. A.G. C.G. C.G.</la3></la3>	
Query Match 100.0%; Score 201; DB Best Local Similarity 100.0%; Pred. No. 2.7e-Matches 34; Conservative 0; Mismatches	3 2; Length 184; 1-17; 0; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLLHACIPCQLRCSSNFPPLTCQRYC 34 	

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A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3
                                                                                                                              30.3%;
ilarity 37.5%;
Conservative
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Similarity 42.9%;
9; Conservative
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ilarity 37.1%;
Conservative
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Best Local Similarity
Matches 13; Conserv
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Best Local
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C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T42215
R;Gao, Z.; Garbers, D.L.
J;Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane profixeence number: 222080; MUID:99123114
A;Ceession: T42215
A;Status: preliminary: translated from GB/EMBL/DDBJ
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A;Experimental source: strain Bristol N2
C;Genetics:
                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 «NAAA
A;Cross-references: GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C;Reywords: hydrolase; serine proteinase
                                                                                                             PC6,
                                                                                                             an extremely large Cys-rich region of
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A;Cross-references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC26680.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16840
R;Geisel, C.
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                      Length 1548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: functions in multiple cell adhesion processes A; Note: found exclusively on the apical region of the sperm head
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T10E10.
A;Reference number: Z18588
                                                                                                                                                                                                                                                                                                                  Score 67.5; DB 2;
Pred. No. 2.3;
; Mismatches 14;
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A, Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DP
A;Residues: 1-1101 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64.5; DB
Pred. No. 16;
5; Mismatches
R; Nakagawa, T.; Murakami, K.; Nakayama, K. FEBS Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an A; Reference number: S34583; MUID:93327934
A; Accession: S34583
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.
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37.8%;
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Best Local Similarity 35.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
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A;Gene: CESP:T10E10.4
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C; Function:
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A; Cross-references: EMBL: U39851; NID: 91055062; PID: 91055068; PIDN: AAA81069.1; CESP: C2
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functional characterization of FURIN from Spodoptera frugi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Function:
A;Description: responsible for the endoproteolytic processing of proproteins with spe
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                furin (EC 3 4.21.75) - fall armyworm
NyAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase;
C;Species: Spodoptera frugiperda (fall armyworm)
C;Species: Spodoptera frugiperda (fall armyworm)
C;Accession: T43251
R;Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A;Description: Cloning and functional characterization of FURIN from Spodoptera fru
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                                                                                                                                                                                                                                                                                     C. Species: Caenorhabditis elegans
C. Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C. Accession: T15577
R. Latrelle, P.
Submitted to the EMBL Data Library, November 1995
A. Description: The sequence of C. elegans cosmid C23G10.
A. Reference number: 218372
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-758 <LAT>
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:C23G10.8
A;Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8
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6
  Length 1101;
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                                                    Indels
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                                                                                                                                                                                                                                                                    hypothetical protein C23G10.8 - Caenorhabditis elegans
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residucs: 1-1299 <CIE>
A,Cross-references: EMBL:268888; NID:91167859; PID:6
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Pred. No. 14;
6; Mismatches
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Pred. No. 28;
5; Mismatches
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                                               7; Mismatches
                                                                                                                          1 CSQNEYFDSLLHACIPCQLR--CSSNTPPLTC 30
Score 61;
Pred. No.
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260 ESVFHPLYPAEIRCSADGPPL 280
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A.Cross-references: EMEL:M86396; NID:q160957; PIDN:AAA29866.1; PID:q160958
A:Note: sequence extracted from NCBI backbone (NCBIP:111129)
C:Genetics:
A:Gene: SER
C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homol
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F:1018-1323/Domain: protein kinase homology <KIN>
F:1026-1034/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Hardy, D. M.; Garbers, D. L.
J. Biol. Chem. 270, 26025-26028, 1995
J. Biol. Chem. 270, 26025-26028, 1995
A; Title: A sperm membrane protein that binds in a species-specific manner to the egg
A; Reference number: 221464; MUID: 96064658
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A; Cross-references: EMBL:U40024; NID:g1066465; PID:g1069466; PIDN:AAC48486.1
A; Experimental source: strain Meishan; testis
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
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A; Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A; Reference number: 214346
                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1717; 48;
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A; Cross-references: EMBL:AF001308; NID:g2104523; PID:g3912931
A; Experimental source: cultivar Columbia
C; Genetics:
A; Map position: 4S
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C.Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text
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C;Function:
A;Description: may be involved in sperm adhesion to the
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R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T10M13.17.1 - Arabidopsis thaliana
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A;Accession: T34027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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86;
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A;Status: translated from GB/EMBL/DDBJ
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31.6%;
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-1717 <SHO>
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Best Local Similarity
Matches 9; Conserv
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Matches 12; Conserv
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                                          C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 19-Mar-1997 sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: 807127
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
R*Babin, D.R.; Peanasky, R.J.; Harden, B. Harden, B. Harden, B. Haphys. 2.32, 143-161, 1984
A;Title: The isolnhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the prima A;Reference number: 807127; MUID:84255715
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A: Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc A;Reference number: A43434; MUID:92381036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cybre: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 10.Sep-1999
Cybrcession: A45558; S27836
RyShoemaker, C.B.; Remachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Blochem. Parasitol. 53, 17.32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Recession: A45588; MUID:92365727
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni) N;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1680 <ROE>
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
C;Genetics:
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C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;409-652/Domain: subtilisin homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                      chymotrypsin/elastase inhibitor - common roundworm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1199 CSESEFYSQVEGQCRPCHASCGSCNGPADTSCTSC 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57.5; DB
Pred. No. 2.5;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHACIPCQLRC--SSNTP-PLTCQR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSQNEYFDSLLHACIPCQLRCSS-NTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 41;
5; Mismatches
                                                                                                                                                                                                                                                              A Status: preliminary
A Molecule type: protein
A; Residues: 1-63 <BAB>
C; Superfamily: roundworm trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.6%;
34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.6%;
Best Local Similarity 37.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: FlyBase: Fur2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: A43434
                                                                                                                                                                                                                                             A; Accession: S07127
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Search completed: June 25, 2002, 16:13:22 Job time: 122 sec
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Best Local Similarity
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                                                                                                                                                                                                                                                                                       hypothetical protein T23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25169
R;Wilkinson, J.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219990
A;Reference number: Z19990
A;Reference number: Z19990
A;Reference number: Z19990
A;Reference number: Z19990
A;Catous: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-330 <WIL>
A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Coss-teferences: EMBL:281573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02G9.1
A;Experimental source: clone M02G9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23681
R;Matthews, L.
                                                                                                                          Gaps
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A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
                                                                              Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1513;
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                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.4%; Score 55; DB 2; Le 44.8%; Pred. No. 75; active 3; Mismatches. 11;
                                                                                  5,
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20;
                                                                                  DB
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Pred. No. 20;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November 1996
A;Reference number: 219781
A;Accession: 723681
                                                                              Score 55.5; DI
Pred. No. 45;
3; Mismatches
                                                                                                                                                                                       1 CSQNEYFDSLLHACIPC----QLRCSSNTPP 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                              Query Match 27.6%;
Best Local Similarity 41.9%;
Matches 13; Conservative
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ilarity 28.6%;
Conservative
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Best Local Similarity 44.8%
Matches 13; Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: T23F1.6
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A; Introns: 31/3
A; Note: T10M13.17.1
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A;Introns: 16/3
C;Superfamily: qli
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Gaps

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26.9%; Score 54; DB 2; Length 1980; 52.9%; Pred. No. 1.2e+02; Live 2; Mismatches 6; Indels

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C; Species: Rattus norregicus (Norway rat)
C; Species: Rattus norregicus (Norway rat)
C; Species: Rattus norregicus (Norway rat)
C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C; Caccession: 554307
R; Rainhard, J: Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J: 14, 697-704, 1995
A; Title: A novel type of myosin implicated in signalling by rho family GTPases.
A; Reference number: 554307; MulD: 95188874
A; Reference number: 554307
A; Status: preliminary; nucleic acid sequence not shown
A; Residues: 1-1980 (REL)
A; Residues: 1-1980 (REL)
A; Residues: 1-1980 (REL)
A; Cross-references: EMBL: 77609; NID: 9639999; PIDN: CAA54700.1; PID: 9639999
C; Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C
C; Keywords: nucleotide binding; P-loop
F; 149-942/Domain: myosin motor domain motif A (P-loop)
F; 239-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>
                            C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C.Accession: T30197
R.Legan, P. K.; Rau, A.; Keene, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A.Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to A; Reference number: 220771; MUID: 97236843
A.Accession: T30197
A.Accession: T30197
A.Accession: T30197
A.Mocelule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-2155 <-LEGA
A.Cross-references: EMBL: X99805; NID: 91915908; PIDN: CAA68138.1; PID: 91915909
A.Experimental source: strain CD1; whole cochleae
A.Note: non-collagenous protein only expressed in the inner ear, by cells both in and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

27.1%; Score 54.5; DB 2;
Best Local Similarity 29.4%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | :::| : | | | |::
1372 CPPNSHYESCVSVCQP---RCAAIRLKSDCNHYC 1402
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alpha tectorin - mouse
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 25, 2002, 16:22:41; Search time 27.55 Seconds (without alignments) 47.785 Million cell updates/sec Run on:

US-09-854-864-7 201 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters:

105224 segs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	002223 homo sapien 004592 mus musculu 088799 mus musculu 088799 mus musculu 088799 mus musculu 087032 drosophila 029813 usu scrofa 09ult0 homo sapien 063358 rattus norv 099706 mus musculu 013459 homo sapien 029537 canis famil 039529 saccharomyc 097430 mus musculu 0286537 canis famil 028655 mus culiu 028065 bos taurus 028065 bos taurus 08225404 mirabilis j 028065 bos taurus 08225404 mirabilis j 028065 bos taurus 082255 sus scrofa 093316 homo sapien 09015 branchiosto 09015 sus scrofa 03316 homo sapien 09015 branchiosto 09088 caenorhabdi 043316 homo sapien 09088 caenorhabdi 043316 sus scrofa 091088 caenorhabdi 043316 sus scrofa 091055 sus scrofa 091055 sus scrofa 091065 sus saccharomyc 0910705 mus musculu 061001 mus musculu
SUMMARIES	TE17 HUMAN PCK5_MOUSE SSPO_BOVIN ICE1_ASCSU EXN_MOUSE SSPO_BOVIN ICE1_ASCSU ZAN_MOUSE ZAN_BTG YN2_DROME ZAN_BTG WY9B_HUMAN WY9B_MOUSE WY9B_HUMAN WY1A_HUMAN WY1A_HUMAN WRC1_CAEEL PAX4_HUMAN WRC1_CAEEL WAC1_CAEEL WAC1_CAEEL WAC1_CAEEL WAC1_CAEEL WAC1_CAEAT WRC1_CAEAT WRC1_CAEAT WRC1_CAEAT WRC1_MOUSE IMA5_MOUSE IMA5_MOUSE IMA5_MOUSE IMA5_MOUSE IMA5_BOVIN ALB1_SALSA ITR4_RADMA TEP1_MACMU
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Score	
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P27966 avian rous- 043865 homo sapien P41990 caenorhabdi 091448 homo sapien P29122 homo sapien P29122 homo sapien P349122 homo sapien P41885 felis silve P5268 homo sapien P41885 felis silve P5268 homo sapien P91127 glardia lam 009807 schizosacch Euteleostomi; e; Homo. rger R., interleukin 2 gene T cell lymphoma."; T cell lymphoma.";	andon R., chell S., Chell S., DNA sequence from Tokunaga K.; ases. , Madry C.,) associates with TRAF3 and e, and p38
34 48 23.9 450 1 RMIL_AVEVR 35 48 23.9 500 1 SAH2_HUMAN 36 48 23.9 500 1 SAH2_HUMAN 38 48 23.9 515 1 APX1_CAEEL 38 48 23.9 581 1 LDLC_CAREL 39 48 23.9 902 1 UBPF_HUMAN 40 47.5 23.6 355 1 AMBP_PLEPL 41 47.5 23.6 356 1 PAC4_HUMAN 42 47.5 23.6 1798 1 LMB2_HUMAN 47 23.4 349 1 VC22_VARV 45 47 23.4 349 1 VC22_VARV 46 47 23.4 587 1 VSA1_GIALA 47 23.4 687 1 VSA1_GIALA 48 47 23.4 7 1 1 YAB5_SCHPO ALIGNMENTS SULT 11_HUMAN STANDARD; PRT; 184 AA. 00.20223; 01-JUL-1993 (Rel. 26, Last sequence update) 01-MAX-2002 (Rel. 41, Last annotation update) 01-MAX-2002 (Rel. 41, Last annotation update) 01-MAX-2002 (Rel. 41, Last annotation update) 01-MAX-2002 (Rel. 41, Last sequence update) 01-MA	, B . , Mi. Mi. Mi. Mi. Mi. B

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FEBS Lett. 327:165-171(1993).
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004552; 062040;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation envertase PC5)
(Convertase PC5) (PC6) (Subtilisin-like proprotein convertase 6)
                     Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moroe M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Harrison K., Kindsvogel W., Clegg C.H.;

"TACI and BCMA are receptors for a TNF homologue implicated in B-cell autolimmune disease.";
                                                                                                              -!- FUNCTION: RECEDED FOR THESF13B/BLYS/BAFF.
-!- TISSUE SPECIFICITY: EXPRESSED IN MATURE B-CELLS.
-!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa T., Murakami K., Nakayama K.;
"Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Proto-oncogene; Transmembrane; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           BREAKPOINT FOR TRANSLOCATION TO FORM
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_012234.
277AF11E2767D932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 201; DB 1; 100.0%; Pred. No. 4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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             MEDLINE=20259066; PubMed=10801128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ICR; TISSUE-Intestine;
MEDLINE-93327934; PubMed-8335106;
                                                                                                                                                                                                                                                                                               EMBL, 214954; CAA78679.1; -. BMBL, 229575; CAA88591.1; -. EMBL, 229574; CAA82691.1; -. EMBL, U95742; AA867251.1; -. EMBL, U95742; AA867251.1; -. PIRE, S31208; S31208.
                                                                                                                                                                     WHICH INVOLVES BCMA AND IL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AA; 20138 MW;
                                                                                                      Nature 404:995-999(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism.
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                          109545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCK5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCSK5
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g
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AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.

AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.

-1-TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST ABUNDANT IN THE INTESTINE AND ADDRENALS.

PURBERIALS. ADRENALS AND LUNG BUT NOT IN THE BRAIN.

-1-DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO.

EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER, BUT MARKEDLY UPREGULATED A DISCRETE SITES DURING DEVELOPMENT. AT E5.5, FROMINENT EXPRESSION IN EXPRESSION IN DIFFERENCIATED DECIDUA. AT E7.5, INTENSE EXPRESSION IN EXPRESSION IN SOMITES AND YOLK SAC FOLLOWED BY A CONFINATION TO DERMANOTOME COMPARTMENT. BETWEEN E9.5 AND BILS. ABUNDANT EXPRESSION IN SOMPRESSION IN SETWEEN E9.5 AND YOLK CELLS OF LIMB BUDS). AT E1.5, EXPRESSION IN THE LIMBS IS CONFINED TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rancourt S.L., Rancourt D.E.;
"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, sonitogenesis, and skeletal formation.";

Dev. Genet. 21:75-81(1997)

-!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLENVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORPEX VIA THE ACTIVATION OF OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPORTEINS BY CLEAVAGE OF ARG-YAA-YAA-ARG-1-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
MEDLINE-97103178; PubMed-8947550;
Be lie I., Marchitewicz M., Malide D., Lazure C., Nakayama K.,
Bendayan M., Seidah N.G.;
"The isoforms of proprotein convertase PC5 are sorted to different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL EXPRESSION.
MEDLINE-96293359; PubMed-8698813;
Constam D.B., Calfon M., Robertson E.J.;
"SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis.";
J. Cell Biol. 134:181-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G., "CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells.".

Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                                                                                                                                                                mammalian Kex2-11ke processing endoprotease family: its striking
structural similarity to PACE4.";
J. Biochem. 113:132-135(1993).
                                                                                                                                                                                                                                        "Identification and functional expression of a new member of
SEQUENCE FROM N.A. (ISOFORM PC5A).
ISSUE-Brain, and Intestine.
MEDLINE-93224489; Pubmade-8468318;
Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM PC5A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subcellular compartments.";
J. Cell Biol. 135:1261-1275(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Adrenal cortex;
MEDLINE-93342056; PubMed-8341687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL EXPRESSION.
MEDLINE-97436919; Pubmed-9291583;
                                                                                                                                                                                            Nakayama K.;
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ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.

DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
                                                           DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS WITH THE TGN SORTING PROTEIN PACS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                Property Products: Peptidase_S0.

Pram: PF00483; Pr. 1.

Pram: PF00482; Peptidase_S8; 1.

Pram: PF00082; Peptidase_S8; 1.

Probom: PD000717; P_domain; 1.

SMART; SM00181; EGF_3.

SMART; SM00181; EGF_11ke; 2.

SMART; SM00181; EGF_11ke; 2.

PROSITE; PS00136; SUBTILASE_ASP; 1.

PROSITE; PS00138; SUBTILASE_HIS; 1.

PROSITE; PS00138; SUBTILASE_ER; 1.

HydroLase; Serine protease; Glycoprotein; Zymogen; Signal;

Cleavage on pair of basic residues; Repeat; Alternative splicing;
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(BY SIMILARITY).
(BY SIMILARITY).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                       ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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N-LINKED (GLCNAC.
                                                                                                                              SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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N-LINKED
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InterPro; IPR00174; Furin-like.
InterPro; IPR002884; P_domain.
InterPro; IPR000209; Peptidase_S8.
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667
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PIR; JX0248; JX0248.
PIR; A48225; A48225.
HSSP; Q99405; IMPT.
MEROPS; S08.076; -.
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ACT_SITE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE ZONA PELLUCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXCLUSIVELY ON THE
                                                                                                                                                                                                Gaps
                                    SPIQEDCISCPVIRVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SÜBÜNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SÜBÜLLÜLAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.
-!- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HALOID SPERMATIDS.
-!- DOMAIN: THE MAM DOWAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.
                N-LINKED (GLCNAC. ..) (POTENTIAL).
GEYIDDQGHCQTCEASCAKCWGPTQEDCISCPVTRVLD
ATEESWAEGGFCMLVKKNNLCQRKYLQQLCCKTCTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCHAL ISTHMUS.
-i- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-i- SIMILARITY: CONTAINS 3 MAN DOMAINS.
-i- SIMILARITY: CONTAINS 12 SVWFD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                              .;
2
                                                                                                                                                             Length 1877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ON AND/OR
                                                                                                                                                                                              ndels
                                                                     (IN ISOFORM PC5A).
MISSING (IN ISOFORM PC5A).
MW; EC850E2DF20EA1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION
N-LINKED (GLCNAC. . .
                                                                                                                                                                                              14;
                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                 1481 CAAVEYWDEGSHRCQPCHKKCSRCSGPSEDQCYTCPR 1517
                                                                                                                                                                                                                                                                                                                                                  ZAN_MOUSE STANDARD; PRT; 5376 AA. 088799; 008647; 16-07-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                             1 CSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQR 32
                                                                                                                                                         Score 67.5; DI
Pred. No. 0.5;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domains.";
J. Biol. Chem. 273:3415-3421(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Testis;
MEDLINE-98123114; PubMed-9452463;
Gao Z., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                                              4,
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                                                                                                                                                           33.6%;
37.8%;
                                                                                    916 1877
1877 AA; 209287
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conadhesin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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CARBOHYD
CARBOHYD
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SEQUENCE
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Best Local 8
                                  /ARSPLIC
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MEDLINE-9638614; PubMed-8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,
Lamalle D., Dastugue B., Meiniel A.;
"SCO-spondin: a new member of the thrombospondin family secreted by
the subcommissural organ is a candidate in the modulation of neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
01-007-19901 (Rel. 40, Last annotation update)
SCO-spondin (Fragment).
Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggregation.";

1. Cell Sci. 109:1053-1061(1996).

1. FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.

1. SUBCELLULAR LOCATION: Extracellular.

1. TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.

1. SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

1. SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.

1. SIMILARITY: CONTAINS AT LEAST 1 EAST 2 EGF-LIKE DOMAINS.

1. SIMILARITY: CONTAINS AT LEAST 3 LEAST 1 EAST 3 LDL-RECEPTOR CLASS A DOMAINS.
                                                                (POTENTIAL)
(POTENTIAL)
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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                      GECNAC
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Matches 13; Conservative
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PROSITE; PS01186; EGF_2: 18.
PROSITE; PS00740; MAM_1; FALSE_NEG.
PROSITE; PS50066; MAM_2; Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
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InterPro; IPR0003645; Foln.
InterPro; IPR001998; MAM.
InterPro; IPR001919; TIL.
InterPro; IPR001007; VWFC.
INTERPOO094; VWG. 4.
SMART; SM00111; EGF; 2.
SMART; SM00111; EGF; 2.
SMART; SM00114; VWC; 17.
SMART; SM00214; VWC; 17.
SMART; SM00214; VWC; 17.
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BR InterPro: IPR00172; LbL_recept_A.

BR InterPro: IPR00172; LbL_recept_A.

BR InterPro: IPR00184; TSP1.

BR Ffam: PF000185; TIL; 1.

BR Ffam: PF000185; TIL; 1.

BR Ffam: PF000185; TSP1.

BR SMART: SM00192; LDLA: 3.

BR SMART: SM00192; LDLA: 3.

BR SMART: SM00192; LDLA: 3.

BR SMART: SM00186; FSP1.

BR SMART: SM00186; LDLA: 1.

BR ROSITE: PS01286; PS81.

BR ROSITE: PS01286; DLRA-1; 3.

BR ROSITE: PS50092; TSP1; 4.

BR ROSITE: PS50092; TSP1; 4.
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=92381036; PubMed=1512259;
Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
Cloning and functional expression of Dfurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with multiple
repeats of a cysteine motif.";
J. Biol. Chem. 267:17208-17215 (1992).
J. Biol. Chem. 267:17208-17215 (1992).
ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Opptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chymotrypsin/elastase isoinhibitor 1 (C/E-1 inhibitor).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides)
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
NCBI_TaxID=6253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A TATAL CATALALOGAMENT (2.4 MANOSTROMS) OF COMPLEX WITH ELASTASE.

A MEDLINE-56006335; PubMed-7922044;

Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;

T chymotrypsin/elastase of the complex of Ascaris

- Chymotrypsin/elastase inhibitor with porcine elastase.";

Structure 2:679-689(1994).

C -!- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.

-!- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.

-!- SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.

R PDB; 1EAI; 05-APR-99.

R PIRS, 207127; 207127.

R PFdm, PF01826; TIL, 1.

Serine protease inhibitor; 3D-structure.

5 38

T DISULFID 14 33

T DISULFID 17 29

T DISULFID 17 29

T DISULFID 21 60

T DISULFID 31 32

R REACTIVE BOND.

SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 63;
                                                                                                                                                                                                                                                                                                                 SEQUENCE.

MEDLINE=84255715; PubMed=6564898;
Babin D.R., Peanasky R.J., Goos S.M.;
The isolnhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure.";
Arch. Blochem. Blophys. 232:143-161(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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Pred. No. 0.41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
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37.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 37.1
Matches 13; Conservative
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1 CSQNEYFDSLLHACIPCQLRCSS-NTPPLTCQRYC

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                      proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin,
                                                                                        respective precursors.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY. FURIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FURIN-LIKE PROTEASE 2.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
10 X TANDEM REPEATS, CYS-RICH.
                                                                  component C3 and von Willebrand factor from their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0136; SUBTILASE_ASP; 1.
PROSITE; PSO0137; SUBTILASE_HIS; 1.
PROSITE; PSO01318; SUBTILASE_ERS; 1.
Hydrolase; Serine processe; Glycoprotein; Signal; Transmembrane; Multigene family; Zymogen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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(POTENTIAL).
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CATALYTIC ACTIVITY: Release of mature proteins from their
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(GLCNAC...)
(GLCNAC...)
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CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC. . .)
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HSSP, 099405; IMPR-
Flybase; FBGN0004598; Fur2.
InterPro; IPR0001474; Futh-like.
InterPro; IPR00214; Futh-like.
InterPro; IPR002184; P. domain.
InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00757; Furin-like; 1. Pfam; PF00787; Furin-like; 1. Pfam; PF001482; Pp 1. Pfam; PF00082; Peptidase_S8; 1. PRINTS; PR00723; SUBTILISIN. SMART; SM0181; EGF; 1. SMART; SM00261; FU; 10.
                                                                                                                                                                                                                                                                                                                                                     EMBL; M94375; AAA28551.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAR REGION OF THE SPERM HEAD (BY STRILARTY).

-1. TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDINIS.

-1. DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.

-1. DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE DOMAIN MIGHT INHIBIT TRAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.

-1. DOMAIN: THE VWED DOMAINS AND THE MUCIN-LIKE DOMAINE OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.

-1. PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1. Biol. Chem. 270:26025-26028(1995).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                    manner
                                                                                                                                                                              Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 823-830, 859-872; 883-890 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1921. STRAIN=MEICHAN; TISSUE-TGE418; MEDLINE-96064658; PubMed-7592795;
                                                                                                                                                                                                                                                                                                                                                                        "A sperm membrane protein that binds in a species-specific m
the egg extracellular matrix is homologous to von Willebrand
factor.";
                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                      PRT; 2476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 2 MAM DOMAINS. SIMILARITY: CONTAINS 4.5 VWFD DOMAINS. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000561; EGF-11ke.
InterPro; IPR000599; MAM.
InterPro; IPR002919; TIL.
InterPro; IPR001328; TIL.
InterPro; IPR001007; VWFC.
InterPro; IPR001007; VWFC.
InterPro; IPR001846; Vwd.
Pfam; PF00629; MAM; 2.
Pfam; PF001826; TIL; 5.
Pfam; PF00184; Vwd.
Spfam; PF00184; Vwd.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                             Hardy D.M., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U40024; AAC48486.1;
                      STANDARD;
                                                                                                                        Zonadhesin precursor.
                                                                                                                                                              scrofa (Pig).
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                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNALING.
                  ZAN_PIG
Q28983;
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ZAN_PIG
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Gaps

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17;

Score 57.5; DB Pred. No. 8.5; 5; Mismatches

28.6%; ilarity 34.3%; Conservative

Ouery Match Best Local Similarity Matches 12; Conserv

5,

DB 1; Length 1680; Indels Nomura N.,

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-!- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN HYRRACELTULAR MOVEMENTS.
MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS
ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                           "Characterization of cDNA clones selected by the GepeMark analysis from size-fractionated cDNA libraries from human brain."; DNA Res. 6:329-336(1999).
-!- SIMILARITY: CONTAINS 8 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reinhard J., Scheel A.A., Diekmann D., Hall A., Ruppert C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley; TISSUE-Brain stem, and Spindl cord; MEDLINE-95188874; PubMed-7882973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR 8.
8B93440B522CFC1C CRG64;
                                                                         TISSUE-Brain;
MEDLINE-20039618; PubMed-10574461;
Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel type of myosin implicated in signalling GTPases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
MYO9B OR MYR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1980 AA
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Pred. No.
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TPR 2.
TPR 4.
TPR 5.
TPR 5.
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InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 7.
PFAMT; SM00028; TPR; 3.
Hypothetical protein; Repeat; TPR
NON TER
REPEAT 264 297 TPR
REPEAT 264 297 TPR
REPEAT 347 381 TPR
REPEAT 415 TPR
REPEAT 415 TPR
REPEAT 415 TPR
REPEAT 415 TPR
REPEAT 630 662 TPR
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38.2%;
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Best Local Similarity
Matches 13; Conserv
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                                                      SEQUENCE FROM N.A.
             NCBI_TaxID=9606;
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063358;
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SWART; SM00137; MAM; 1.
SWART; SM00214; VWC; 2.
SWART; SM00216; VWD; 4.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01166; EGF_2; 4.
PROSITE; PS00740; MAM_1; 1.
Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                        53 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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1; AA SEQUENCE).
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MW; A13B690375A6548C CRC64;
                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                   WWFD 1 (PARTIAL).
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16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA1140 (Fragment).
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8; Mismatches
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BY SIMILARITY.
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VWFD
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31.6%;
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Best Local Similarity 31.6
Matches 12; Conservative
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ID YB40_HUMAN
AC Q9ULTO;
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SIGNAL
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Gaps

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ndels

by rho family

PRT; 2114 AA

STANDARD;

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002706; 090707; 090708; 090709; 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last amnotation update)
Myosin IXb (Unconventional myosin-9b).
                                                                              MYO9B OR MYR5
  MY9B_MOUSE
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
g; Calmodulin-binding; Actin-binding;
GTPase activation; Phorbol-ester binding;
                                                                                       -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOWAIN.
-!- SIMILARITY: CONTAINS 1 GAP DOMAIN.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 4 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAIL.
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
ACTIN-BINDING.
10 1.
10 2.
10 3.
10 4.
PHORBOL-ESTER AND DAG BINDING.
GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1; Length 1980;
Pred. No. 28;
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D79FEC4D0FAE0C05 CRC64;
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NECK OR REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00109; C1; 1.
SMART; SM00109; IQ; 3.
SMART; SM00242; MYSC; 1.
SMART; SM00314; RA; 1.
SMART; SM00314; RA; 1.
PROSTITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSTITE; PS50081; DAG_PE_BIND_DOM_2; 1.
                                                                                                                                                                                                                                                                                                                              Interpro; IPR000159; RA.
Interpro; IPR000198; RhoGAP.
Interpro; IPR001609; myosin_head.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF000612; IQ; 4.
Pfam; PF00063; myosin_head; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00620; RhoGAP; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 2.
                                                                                                                                                                                                                                                                                                      InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000048; IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225035 MW;
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Cytoskeleton; Coiled coil; G7
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1002 10
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1593 16
1673 18
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.
MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSRELETON, BINDS
ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLCALIZES WITH
E-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS
LOCALIZITION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE
PRINTULLERS REGION (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 3 ISOSORMS: 1 (SHOWN HERE), 2/Q AND 3/C ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00242; MISC.,
SMART; SM00342; MISC.,
SMART; SM00314; RA; 1.
SMART; SM00324; RhoGAP; 1.
PROSITE; PSS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PSS00961; DAG_PE_BIND_DOM_2; 1.
PROSITE; PSS00961; DG_3.
PROSITE; PSS00961; DG_3.
PROSITE; PSS00961; DG_3.
PROSITE; PSS00961; ATP-binding; Calmodulin-binding;
                                                                                                                                                                                                                                                                           Grewal P.K., Jones A.-M., Maconochie M., Lemmers R.J.F., Frants R.R., Hewitt J.E.;
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN, HEART, MUSCLE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INNER EAR.
-!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING DOMAIN.
--- SIMILARITY: CONTAINS 1 GAP DOMAIN.
--- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
--- SIMILARITY: CONTAINS 4 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                  "Cloning of the murine unconventional myosin gene Myo9b and
                                                                                                                                                                                                                    SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS
                                                                                                                                                                                                                                                                                                                                   identification of alternative splicing.";
Gene 240:389-398(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF143685; AAF00120.1; -- EEBL, AF143686; AAF00121.1; ALT_FRAME. EMBL; AF144583; AAF00118.1; -- HSSP; P08799; IMMN.
                                                                                                                                                                                                                                                         MEDLINE=20047919; PubMed=10580159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000198; RhoGAP.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:106624; MyO9b.
InterPro; IPR002219; DAG_PE-bind
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Pfam; PF00788; RA; 1.
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SMART; SM00015; IQ; 4.
SMART; SM00242; MYSC; 1.
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                                                                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                   NCBI_TaxID=10090;
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Gaps

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Indels

Mismatches

Conservative

Best Local Similarity Matches 9; Conserv

Query Match

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MY9B_MOUSE RESULT

26.9%; 52.9%;

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RRQDQVHSVYIAPGADLPSQSTLIALDHDTILPGTKRRYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPAPALPCPISPILSPLPEAAAPPRGRPTSFVTVRVKTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grewal P.K., Jones A.-M., Maconochie M., Lemmers R.J.F., Frants R.R.,
                                                                                                                                                                                                                                                                                                                                                                  R -> RCTGLDFSFERSELDVNAFEDIMAFYESR (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1940-2158 FROM N.A. (LONG ISOFORM).
MEDLINE-98158729, Pubmed-94490638;
Post P.L., Bekcch G.M., Mooseeker M.S.;
"Human myosin-IXD is a mechanochemically active motor and a GAP for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPTYCLPPSSGQANG -> E (IN ISOFORM 3).
L -> LEVSPVLPSSSL (ONLY IN STRAIN
C57B1/6; CONTAINS AN IN-FRAME 33 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB-Liver, and Small intestine;
MEDLINE-29063843. Pubmed-8907710;
Wirth J.A.; Jease M.A.; Post P.L., Bement W.M., Mooseker M.S.;
"Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase-activating protein domain in its tail.";
J. Cell Sci. 109:653-661(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 2114; Pred. No. 30;
                                                                                                                                                                                                                                                                                           PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; D774D4B1B2788045 CRC64;
                 HEAD OR MOTOR DOMAIN.
NECK OR REGULATORY DOMAIN.
                                                                      TAIL.
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=20047919; Pubmed=10580159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPERFECT DUPLICATION).
                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MY9B_HUMAN STANDARD; PRT; 2158 AA. 013459; Q9UHN0; 075314; Q9NUJ2; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Myosin IXb (Unconventional myosin-9b).
                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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Gene 240:389-398(1999).
  Polymorphism.
                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      ISOFORM 2)
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TO 2.
TO 3.
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52.9%;
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2114 AA; 238832
Zikc; Alternative splicing;
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                                                                         2114
1592
1859
1945
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977
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1639
1820
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VARSPLIC
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VARSPLIC
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Masuho Y., Kanehori K.;

"NEDO human cDNA sequencing project.";

"NED human contains to the project.";

"NED h
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PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding; Cytoskeleton; Colled coil; Grpase activation; Phorbol-ester binding; Linc; Alternative splicing. HFAD OP WATOR PARATOR
                                             SEQUENCE OF 1828-2023 FROM N.A. (SHORT ISOFORM).

TISSUE-Placenta;

TISSUE-Placenta;

TISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,

Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishib S., Kawai Y.,

Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEAD OR MOTOR DOMAIN.

NECK OR REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF020267; AAC26597.1; -.
EMBL; AK002201; BAA92132.1; ALT_INIT.
HSSP; P08799; 1MND.
MIM; 602129; --
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000048; IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U42391; AAC50402.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000198; RhoGAP.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 2.
Cell Sci. 111:941-950(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00063; myosin_head; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF143684; AAF00119.1;
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SMART; SM00314; RA; 1.
SMART; SM00324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RhoGAP; 1.
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SMART; SM00015; IQ; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00612;
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           ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

OLIGOMERIZATION.

BASIC (REPRESSION OF DNA-BINDING).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

EES -> QEP (IN REF. 2).

L -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95274326; PubMed-7754713;
Purnelle B., Coster F., Goffeau A.;
"The sequence of a 36 kb segment on the left arm of yeast chromosome xidentifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1
 CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
                                                                       SUBGINIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
SUBCELULAR LOCATION: Nuclear.
DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative 86.7 kDa transcriptional regulatory protein in NUC1-NCE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
Saccharomycetales: Saccharomycetaceae: Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    761A718FDC93DA59 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.6%; Score 53.5; E
48.3%; Pred. No. 7;
tive 1; Mismatches
                                                                                                                                                     SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     758
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                                                                                                                                                                                                                                                                                                      EMBL; AF060514; AAC16909.1; --
EMBL; AR020761; BAA78379.1; --
EMBL; S77819; AAA42022.1; --
HSSP; P04637; IOLG
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-oncogene; DNA-binding;
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Pfam; PF00870; P53; 1.
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375
311
380
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356
299
380
                                                              EXPRESSION
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P39529;
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DOMAIN
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CONFLICT
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Matches
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"Aberrations of p53 tumor suppressor gene in various spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEDLINE-9533915; pubmed=7600529; Kraegel S.A., Pazzi K.A., Madewell B.R.; Kraegel S.A., Pazzi K.A., Madewell B.R.; "Sequence analysis of canine p53 in the region of exons 3-8."; "Sequence analysis of canine p53 in the region of exons 3-8."; "Inducence realt. 92:181-186(1995).

-i-,FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANSACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of canine p53 cDNA and detailed characterization of the full length canine p53 protein."; Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID-9615;
                                                                                                                                                                                                                                                                                                                                                                                     ö
         COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ACTIN-BINDING.
1Q 1.
1Q 2.
1Q 3.
1Q 4.
PHORBOL-ESTER AND DAG BINDING.
ACT (POTENTIAL).
PP -> QY (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
WISSING (IN REF. 4).
L. -> P (IN REF. 4).
L. -> P (IN REF. 4).
TVAAPP -> P WEPLH (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                      Length 2158;
                                                                                                                                                                                                                                                           P -> L (IN REF. 3).
P -> S (IN REF. 3).
NG -> MAESHS (IN REF. 3).
W; 4978F1D770F56D28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumors in the dog.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53_CANFA STANDARD; PRT; 381 AA. 029537; Q9TV78; Created) 15-DEC-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53). TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 1;
Pred. No. 30;
}; Mismatches
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MEDLINE=98178696; PubMed=9519881;
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52.9%;
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rosen E., Goldberg I., Hayday A.C.;
"The cloning and characterization of a murine secretory leukocyte
procease inhibitor CDNA."
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MEDLINE-9719310; PubMed=9039268;
Jin F.-Y., Nathan C.F., Radzicch D., Ding A.;
"Secretory laukocyte protease inhibitor: a macrophage product induced by and antagonistic to bacterial lipopolysaccharide.";
Cell 88:417-426(1997).
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MEDLINE-98011992; PubMed-9351627;
Abe T., Tominaga Y., Kikuchi T., Watanabe A., Satoh K., Watanabe Y.,
Nikiwa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ALKI_MOUSE STANDARD; PRT; 131 AA.
P97430; 009081; 009082;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antileukoproteinase 1 precursor (ALP) (Secretory leukocyte protease inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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          reast 10:1235-1249(1994).
-!- SUBCELLUIAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
CLUSTER DOMAIN
                                                                                                                                                                                                                            Threerory IPR00172; 2n_clus; 1.

SMART; SMO0056; GAL4; 1.

PROSITE; PSO0066; GAL4; 1.

PROSITE; PSO0048; ZN2_CY6_FUNGAL_1; 1.

PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.

DNA_BIND 47 73 ZN(2)-CYS(6), FUNGAL_TYPE.

SEQUENCE 758 AA; 86662 MW; 75DA2ECCFI73BE75 CRC64;
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homologues to chromoscme III genes.";
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Pred. No. 13;
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MEDLINE=97271386; PubMed=9126337;
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50.0%;
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908930;

16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last 
                         leukoprotease inhibitor gene in the murine lung.";
Am. J. Respir. Crit. Care Med. 156:1235-1240(1997).
-!- FUNCTION: ACID-STABLE PROTEINASE INHIBITOR WITH STRONG AFFINITIES
FOR TRYPSIN, CHYMOTRYPSIN, ELASTASE, AND CATHERSIN G. MAY PREVENT
ELASTASE-MEDIATED DAMAGE TO ORAL AND POSSIBLY QTHER MUCOSAL
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A57C9E30FE711B8F CRC64;
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-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG, INTESTINE AND PEDIDIOYMIS WITH LOWER LEVELS IN LIVESTICLE. NO EXPRESSION IN BRAIN, HEARY, KIDNEY VESIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
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"Bacterial pneumonia causes augmented expression
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Serine protease inhibitor; Repeat; Signal.
SIGNAL 1 25 BY SIMILARITY.
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InterPro; IPR002221; WAP.
ProDom; PD00195; wap; 2.
ProDom; PD001224; WAP; 1.
SMART; SM00217; WAP; 2.
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131 AA;
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                                                                              Morbald S., Yamazaki H., Bujo H., Kusunoki J., Kanaki T., Seimiya K., Amorsaki N., Nimpf J., Schneider W.J., Saito Y.;

Amorisaki N., Nimpf J., Schneider W.J., Saito Y.;

"A novel mosale protein containing LDL receptor elements is highly conserved in humans and chickens.";

Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).

"I strentoscler. Thromb. Vasc. Biol. 17:996-1002(1997).

"I strentoscler. Thromb. Vasc. Biol. 17:996-1002(1997).

"ANY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES.

BINDS LDL, THE MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA.

AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS. BINDS THE RECEPTOR-ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL

INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK REGILATORY EFFECTS ON THIS RECEPTOR.

"SOBCELLULAR LOCATION: Type I membrane protein (Potential).

"I SUBCELLULAR LOCATION: Type I membrane protein (Potential).

"I STRILARITY: CONTAINS 5 BNR REPEATS.

"SIMILARITY: CONTAINS 1 LGF-LIKE DOMAINS.

"SIMILARITY: CONTAINS 1 LGF-LIKE DOMAINS.

"SIMILARITY: CONTAINS 1 LGF-REEPTOR CLASS A DOMAINS.

"SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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LDL-RECEPTOR CLASS A 2
LDL-RECEPTOR CLASS A 3
LDL-RECEPTOR CLASS A 4
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Interpro; IPR000561; EGF-11ke.
Interpro; IPR000361; FN_III.
Interpro; IPR000172; LDL_recept_A.
Interpro; IPR000033; Ldl_recept_a.
Interpro; IPR000037; Ldl_recept_a: 11.
Pfam; PF000057; Idl_recept_b: 5.
Pfam; PF00058; Idl_recept_b: 5.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00181; EGF; I.
SMART; SM001092; LDLARECEPTOR.
SMART; SM001092; LDLARECEPTOR.
SMART; SM001092; LDLARECEPTOR.
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                                               SEQUENCE FROM N.A.
                         NCBI_TaxID=9031;
                                                         TISSUE=Brain;
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LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 8.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 11.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 11.
LDL-RECEPTOR CLASS A 11.
LDL-RECEPTOR CLASS A 10.

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38.7%;
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Matches 12;
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                                                                                              DOMAIN
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us-09-854-864-7.rsp

a grange of

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 25, 2002, 16:24:25 ; Search time 89.98 Seconds (without alignments) 65.368 Million cell updates/sec Run on:

1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34 US-09-854-864-7 201 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database

sp_archea:* sp_bacteria:*

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertebrate:* sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* sp_bacteriap:* sp_rodent:* sp_virus:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	136	67.7	185	11	088472	088472 mus musculu
7	72.5	36.1	499	11	088714	088714 mus musculu
m	71.5	35.6	249	1	C9DBZ3	Q9dbz3 mus musculu
4	71.5	35.6	249	11	09ET35	Q9et35 mus musculu
S	66.5	33.1	293	4	014836	014836 homo sapien
9	64.5	32.1	5374	11	00N660	O99nd0 mus musculu
7	61	30.3	996	Ŋ	022378	022378 caenorhabdi
8	59.5	29.6	353	S	Q5VW81	Q9vw81 drosophila
σ	59	29.4	937	Ŋ	QSGYR5	09qyr5 caenorhabdi
10	58	28.9	175	11	008060	Qgd8d0 mus musculu
11	58	28.9	1299	Ŋ	026489	Q26489 spodoptera
12	57.5	28.6	62	'n	077419	077419 ascaris suu
13	57.5	28.6	1679	ഗ	Q24301	Q24301 drosophila
14	57	28.4	321	10	C9MAMO	Q9mam0 arabidopsis
15	57	28.4	1717	S	026566	Q26566 schistosoma
16	26	27.9	341	11	090351	Q9d351 mus musculu

Ogpvd4 xenopus lae Ogev80 drosophila Ogve40 drosophila Ogve40 drosophila Ogsdn2 homo sapien Og2u0 arabidopsis Ogvit6 drosophila Ogus3 homo sapien Og2u83 homo sapien Og9u83 callitrichi Ol7970 caenorhabdi Og9u83 callitrichi Ol7970 caenorhabdi Og9u823 homo sapien Ogf031 homo sapien Osf443 homo sapien Osf443 homo sapien Osf443 homo sapien Osf9u77 entamoeba h Ogeo9 hepatitis c Ogeux canis famil Og9u44 drosophila Og9u57 homo sapien Og9u6813 hepatitis c			ECEPTOR SUPERFAMILY,	; Euteleostomi; e; Murinae; Mus.	oglou A., actor Receptor bases.		Itoh M., Ishii Y., achi J., Fukuda S., kawa T., Saito R., S., Casavant T.,	King B., Kochiwa H., Pesole G., Quackenbush J., ta M., Wagner L., Washio T.,	R., Barsh G., Bonaldo M.F., Jariboldi M.,	.ya M., Lee N.H., Mombaerts P.,
17 56 27.9 387 13 Q9PVD4 18 55.5 27.6 146 12 Q9EP28 19 55.5 27.6 225 5 Q9VE40 20 55.5 27.6 955 4 Q9EDN2 21 55.5 27.6 989 10 Q9ZUOD 22 55.5 27.6 989 10 Q9ZUOD 23 55. 27.4 340 11 Q9ZUCD 24 55 27.4 440 1 Q9BUS3 25 27.4 1074 5 Q9EVZ3 26 55 27.4 1127 12 Q99XPD 29 55 27.4 1127 12 Q99XPD 29 55 27.4 1127 12 Q99XPD 30 54.5 27.1 1792 13 C9TPQ 31 54.5 27.1 1792 13 C9TPQ 31 54.5 27.1 1792 13 C9TPQ 32 54.5 27.1 1792 13 C9TPQ 34 54.5 27.1 1792 13 C9TPQ 35 56.0 2447 5 Q9BTPQ 36 57.5 26.0 244 7 5 Q9BTPQ 37 54.5 27.1 2155 11 C9BEPQ 38 53.5 26.6 246 6 Q9TUX4 41 53.5 26.6 246 6 Q9TUX4 42 53.5 26.6 2843 4 Q9EPSZ 44 53.5 26.6 2843 4 Q9EPSZ 44 53.5 26.6 2843 4 Q9EPSZ 44 53.5 26.6 2843 4 Q9EPSZ	ALIGNMENTS	1 8472 PRELIMINARY; 8472; OTTEMBET OF	-NOV-1998 (TEMBLIE: 08, Created) -NOV-1998 (TEMBLIE: 08, Last sequence update) -JUN-2001 (TEMBLIE: 17, Last annotation update -CELL MATURATION PROTEIN (TUMOR NECROSIS FACTOR R RMER 17).	<pre>PRSF17. Is musculus (Mouse). Is musculus (Mouse). Ikaryota; Metazoa; Chordata; Craniata; Vertebrata nmmalia; Eutheria; Rodentia; Sciurognathi; Murida 11</pre>	RP SEQUENCE FROM N.A. RC STRAIN-BALLS/C; TISSUE-SPLEEN; RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzo RA LeConiat M., Mornon JP., Berger R., Tsapis A.; RT "Murine BCMA: a new member of the Tumor Necrosis Fa RY Superfamily."; R. Superfamily."; R. Suberfamily."	RN [2] RP SEQUENCE FROM N.A. RC STRAIN=C57BL/6J; TISSUE=COLON; RV MEDY TWO 21100000000000000000000000000000000000	RX MEDLINE=21085660; Pubmed=11211851; RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M. RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J. RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo \$., RA Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T. RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casa	Fleischmann W., Gaasterland T., Gissi C., Kuehl P., Lewis S., Matsuo Y., Nikaido I. Schriml L.M., Staubli F., Suzuki R., Tomi	Sakai K., Okido T., Furuno M., Aono H., Ba Blake J., Boffelli D., Bojunga N., Carnin Brownstein M.J., Bult C., Fletcher C., Fu	RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kam: RA Lyons P., Marchionni L., Mashima J., Mazzarelli J.

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Ra Alzawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Alzawa T., Jawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Gasterland T., Gissi C., King B., Kochiwa H.,
Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ra Kehl P., Lewis S., Matsuo Y., Nikaido I., Pasole G., Quackenbush J.,
Ra Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
Ra Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21177254; PubMed-10881172;
Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Mature 409:685-690(2001).
EMBL; AR004668; BAB23457.1;
MGD; MGI:1889411; Infrsf13b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
35.6%; Score 71.5; DB 11; Length 249;
Best Local Similarity 35.3%; Pred. No. 0.0038;
Matches 12; Conservative 8; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26981 MW; 6F4290D719FEA037 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.6%; Score 71.5; DB 11;
35.3%; Pred. No. 0.0038;
tive 8; Mismatches 13;
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                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-LUNG;
MEDLINE-21085660; Pubmed-11217851;
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EMBL; AF257673; AAG00081.1; -
MGD; MGI:1889411; Infrsf13b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 35.37
Matches 12; Conservative
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    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K. H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rio M.C.;
"Identification of interactions between trefoil peptides and members of the mucin protein family using the yeast two-hybrid system.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ010752; CAA09343.1;
EMBL; AJ010752; CAA09343.1;
Interpro; IPR001846; Vwd.
Interpro; IPR001846; Vwd.
Pfam: PF01826; TIL: 1.
Pfam: PF00094; vwd: 1.
SMART; SMO0216; VWD: 1.
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse),
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                  Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AF061505, AAC23799.1;
EMBL: AK020247; BAB23738.1;
MGD; MGI:1343050; Tnfrsf17.
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                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                                                                                                        Length 185;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                        20442 MW; 8806352B4FD26A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54190 MW; 04F89EF4F23EE61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GASTRIC MUCIN-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                      67.7%; Score 136; DB 11;
70.6%; Pred. No. 2.9e-13;
tive 2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 AA
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                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 CSQNEYFDHSEGTCVPC-----APPTT 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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01-70N-2001 (TrEMBLrel. 17, C;
01-70N-2001 (TrEMBLrel. 17, Ls
01-DEC-2001 (TrEMBLrel. 19, Ls
1200009E08RIK PROTEIN.
                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 48.3 hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                        185 AA;
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SEQUENCE
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 18.
PROSITE; PS50060; MAM_2; 3.
EGF-like domain; Glycoprotein.
SEQUENCE 5374 AA; 579536 MW; 90D2DBCFE5DE24EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.; "Direct Submission."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; u39644, AAA80360.2; HSSP; P10969; 1WGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The sequence of C. elegans cosmid T10E10.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 102.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000794; Ketoacyl-synt.
InterPro; IPR003571; Snake_toxin.
Pfam, PF041chilin_bind_2; 2.
SMARI: SMO0289; WRI: 12.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64.5; DB 11;
Pred. No. 0.99;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3298 CPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      966 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                               Pfam; PF00629; MAM; 3.
Pfam; PF01826; TTL; 25.
Pfam; PF0245; TTL; 25.
Pfam; PF0246; VWd; 4.
SMART; SM0001; EGF_11ke; 1.
SMART; SM00137; MAM; 3.
SMART; SM00137; MAM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 32.1%;
Best Local Similarity 35.1%;
Matches 13; Conservative 5
                                                            IPR003328; TILa.
IPR001846; Vwd.
                                                                                                   InterPro; IPR001007; VWFC.
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                                                                                                                                                                                                                                                                              SM00216; VWD; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
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                                          InterPro;
InterPro;
InterPro;
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                            InterPro;
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022378;
                                                                                                                                                                                                                                                                              SMART;
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                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-97458245; PubMed-9311921;
Von Bulow G.U., Bram R.J.;
"NF-AT activation induced by a CAML-interacting member of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
"Genomic Basis of Inter- and Intra-species Variation in Zonadhesin
Domain Structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P., Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66.5; DB 4; Length 293;
Pred. No. 0.027;
8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domaited (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.
-- STAIRORS ARACABGAL; -- MGD; MGI:106656; Zan.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AF023614; AAC51790.1; -.
Interpro; IPR001368; TWFR.c6.
PROSITE; PS00652; TWFR_NGFR_1; UNKNOWN_1.
SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSMEMBRANE ACTIVATOR AND CAML INTERACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                 293 AA
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6 CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : : | : | : | : | : | : | : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                                                                                                                                                                                                                                                                                                                                            necrosis factor receptor superfamily."; Science 278:138-141(1997).
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-129/SV;
MEDLINE-21138439; PubMed-11239002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%;
32.4%;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 33.19
Best Local Similarity 32.4 Matches 11; Conservative
                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                    sapiens (Human).
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Length 5374;

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Waterston R.;
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SEQUENCE 93
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Q9D8D0;
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RAMINESOUGHORS, DUNNEDG-10731132;

RAGINES-20156060; PUNNEDG-10731132;

RAGINES-20156060; PUNNEDG-10731132;

RAMINES-20156060; PUNNEDG-10731132;

RAMINES G-1074, RAMINES G-1
                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                         Gaps
                                                                                                       5
                                                                       30.3%; Score 61; DB 5; Length 966; 37.5%; Pred. No. 0.62; ive 7; Mismatches 11; Indels
PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;
                                                                                                                                                                                                                                                                (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                        353 AA
                                                                                                                                                  1 CSQNEYFDSLLHACIPCQLR--CSSNTPPLTC 30
                                                                                        Best Local Similarity 37.5
Matches 12; Conservative
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SEQUENCE FROM N.A.
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                                                                          Query Match
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
2010006P15RIK PROFEIN (BAFF RECEPTOR).
MUSS musculus (Mousa Constant (Mussulus (Mousa Constant (Mussulus (Mousa Constant (Mussulus (Mousa Constant (Mussulus (Mussulus Constant (Mussulus
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                                                                                                                                                                                                                                                Length 353;
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                                                                                                                                                                                                                                      Score 59.5; DB 5; Length 3
Pred. No. 0.39;
4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Latraille P., Wohldmann P., Zidanic M.;
"The sequence of C. elegans cosmid C23310.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U39851; AAF99879.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1 protein.
937 AA; 106668 MW; 1C140595DFD3ACE4 CRC64;
Pfam; PF01607; Chitin_bind_2; 4.
SWART; SW00494; ChtBb2; 3.
SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 CSVGNYFDPARRACLPVAISAAHQCSCVLPDNATLANPSDCETY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHACIPCQL----RCSSNTP-----PLTCQRY 33
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 106.7 KDA PROTEIN.
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MEDLINE-99069613; Pubmed-9851916;
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                                                                                                                                                                                                                                                29.6%;
31.8%;
                                                                                                                                                                                                                                      Query Match 29.6'
Best Local Similarity 31.8'
Matches 14; Conservative
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Best Local Similarity 42.5.
Conservative
Comp
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Caenorhabditis elegans.
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OOX RESPECTATION OOX RE

Length 1299;

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Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
Ascarididae; Ascaris.
NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98297373: pubMed=9635450;
Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
Lu C.C., nguyen T., Morris S., Hill D., Sakanari J.A.;
"Anisakis simplex: mutational bursts in the reactive site centers of serine protease inhibitors from an ascarid nematode.";
Exp. Parasitol. 89:257-261(1998).
EMBL: U94499; AAG61300.1;
HSSP; P07851; IEAI.
                                                                                                                                                                                                                                                                                                              4C3799C7BBC572AB ¢RC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CHYMOTRYPSIN/ELASTASE INHIBITOR-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154CE25A375E0B2C CRC64
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
28.6%; Score 57.5; DB 5;
Best Local Similarity 37.1%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 5;
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1150 CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCS----SNTPPLTC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1679 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                   InterPro: IPR002174; Furin-like.
InterPro: IPR00209; Peptidase_S8.
InterPro: IPR00284; P_domain.
Fam; PF001483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF00082; Peptidase_S8; 1.
ProDom; PD000712; SUBTILISIN.
ProDom; P
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FUR2 OR DFUR2 OR CG4235 OR CG18734.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                              PROSITE: PS00136; SUBTILASE ASP.
PROSITE: PS00137; SUBTILASE_HIS;
PROSITE; PS00138; SUBTILASE_SER;
                                                                                                                                                                                                                                                                                                              1299 AA; 142020 MW;
                                                                                                                                                                                                                                                                                                                                                                                 28.9%;
ilarity 37.1%;
Conservative
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Pfam; PF01826; TIL; 1.
NON TER 1
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Best Local Similarity
Matches 13; Conserv
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       MEROPS; SOB.UPB;
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SEQUENCE
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Q24301;
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                                                             STRAIN-C57BL/63; TISSUE-SMALL INTESTINE;

MEDLINE=21085660; PubMed=11217851;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Rsukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rieischmann W., Gaasterland T., Hissi C., King B., Kochiwa H.,

Rieischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,

Ruchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bronstein M.J., Bult C., Fletcher C., Fullita M., Wansho T.,

Ruchons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyishaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kohtsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kohtsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kohtsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kohtsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kayatsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kayatsuki S.,

Nashina M., Wang K.H., Wang K. K., Kawaji H., Kayatsuki S.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Amphipyrinae; Spodoptera.
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TISSUB-SF9, FALL ARMYWORM OVARY;
Cieplik M., Klenk H.;
"Cloning and functional characterization of FURIN from Spodoptera frugiperda (Sf9) cells.";
Sobmitted (JAN-1996) to the ENBL/GenBank/DDBJ databases.
EMBL; Z68888; CAA93116.1; --
HSSP; Q99405; IMPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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NCBI_TaxID=10090;
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026489
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Length 62; Indels ï

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Secret R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batla J.E., Rayler E.G., Helt G., Nolson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Besson K.Y. Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis R.C., Butcher M.R., Bouck J., Brokstein P., Brottier P.,
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RA Burtis R.C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Chenton K., Doup L.E., Downes M., Dugan-Rocha S., Dunkoy B.C.,
Dough L.E., Downes M., Dugan-Rocha S., Dunkoy B.C.,
RA Burtis N.L., Harvey D., Helman T.J., Herrandez J.R., Hostin D.,
Houston K.A., Harvey D., Helman T.J., Herrandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Weirmander J.R., Hostin D.,
Houston K.A., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Mullshina N.V., Morinceh T.C., McLeod M.P., Noshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nesheeb M.G.,
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Raplazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Wang X.,
Spier E., Spradling A.C., Stapleton M., Stupog R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Stupog R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Stupog G., Zhao Q., Zhao Q.
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roebrock A.J., Creemers J.W., Pauli I.G., Kurzik-Dumke U., Rentrop M., Gateff E.A., Leunissen J.A., de Ven W.J.;
"Cloning and functional expression of Diurin2, a subtilisin-like proprotein processing enzyme of Drosophila melanogaster with multiple repeats of a cystelm emotif";
J. Biol. Chem. 267:17208-17215(1992).
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"The Dfur2 gene of Drosophila melanogaster: genetic organization,
expression during embryogenesis, and pro-protein processing activity
of its translational product Dfurin2.";
DNA Cell Biol. 14:223-234(1995).
EMBL, AG005502, AAF46598.1;
ESMBL, L38331, AAF69660.1;
HSSP; Q99405; 1MPT.
                                                                                                                                                            MEDLINE-20196006; PubMed-10731132;
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FlyBarses, FBgn0004598, Fur2.
InterPro, IPR00251, EGF-like.
InterPro, IPR002174; Furin-like.
InterPro, IPR00209; Peptidase_S8.
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MEDLINE-92381036; PubMed=1512259;
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                                                                                                                SEQUENCE FROM N.A.
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                                                                      NCBI_TaxID=7227;
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Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., El J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Byan P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence for Arabidopsis thaliana BAC T25K16 from chromosome
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                                                                                                                                                                3F9E749F0B021CF6 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                         28.6%; Score 57.5; DB 5;
llarity 34.3%; Pred. No. 3.8;
Conservative 5; Mismatches 17;
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                                          Pfam; PF00082; Peptidase_S8; 1. PRINTS; PR00723; SUBTILISIN. PLODOM; PD000717; P_domain; 1. SWART; SM00181; EGF: 1. SWART; SM00261; FU; 10. PROSITE; PS00137; SUBTILASE_ASP; 1. PROSITE; PS00137; SUBTILASE_HIS; 1. SEQUENCE 1679 AA; 183368 MW; 3F
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InterPro; IPR002884; P_domain. Pfam; PF00757; Furin-like; 1. Pfam; PF01483; P; 1.
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Best Local Similarity
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=PUERTO RICAN;

KA MEDIANE-92265727; PubMed=1501637;

Shoemaker C.B., Ramachandran H., Landa A., dos Reis M.G., Stein L.;

Shoemaker C.B., Ramachandran H., Landa A., dos Reis M.G., Stein L.;

Alternative splicing of the Schistosoma mansoni gene encoding a promotogue of epiddermal growth factor receptor.";

Mol. Biochem. Parasitol. 53:17-32(1992).

RMB1, M86396; AAA29866.1; -.

RMB1, M86396; AAA29866.1; -.

RMSP; Pl162; IPR00019; EUR_PRInase.

RICEPTO: IPR00019; EUR_PRInase.

RICEPTO: IPR001245; TYL_PRInase.

RICEPTO: IPR001245; TYL_PRInase.

RICEPTO: IPR001245; TYL_PRInase.

RICEPTO: IPR001245; TYL_PRInase.

RICEPTO: IPR001245; TYL_C.11.

Pfam; PF00059; pkinase; 1.

RMRT; SM00261; FU; 6.

SMART; SM00261; FU; 6.

RMART; SM00261; FU; 6.

RMART; SM00109; PROTFIN KINASE_TYR; 1.

RROSITE; PS00109; PROTFIN KINASE_TYR; 
                                                                                                   Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6183;
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28.4%; Score 57; DB 5; Length 1717;
Best Local Similarity 40.9%; Pred. No. 4.6;
Matches 9; Conservative 2; Mismatches 11; Indels
01-DEC-2001 (TremBlrel. 19, Last annotation update) EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR.
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Search completed: June 25, 2002, 16:24:27 Job time: 657 sec

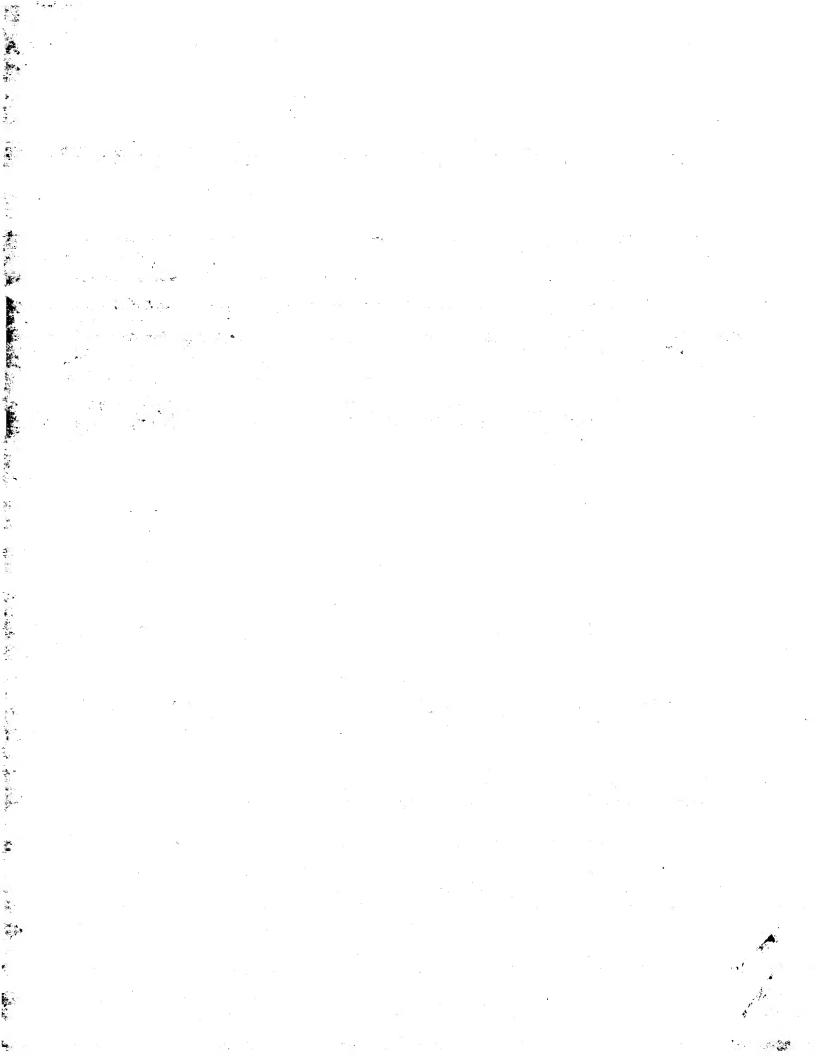
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 25, 2002, 16:16:08; Search time 88.08 Seconds Run on:

(without alignments)
42.876 Million cell updates/sec

US-09-854-864-7 201 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC score: Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A. Sinisal, geneseq/geneseqp-embl/AA1980.DAT:*

Sinisal, gegdata/geneseq/geneseqp-embl/AA1981.DAT:*

Sinisal, gegdata/geneseq/geneseqp-embl/AA1981.DAT:*

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Sinisal, gedata/geneseqgp-embl/AA1991.DAT:*

Sinisal, gedata/geneseqgp-embl/AA1999.DAT:*

Sinisal, gedata/geneseqgp-embl/AA1999.DAT:* A_Geneseq_032802:* 14: 116: 117: 118: 119: 22:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query	Query			
No.	Score	Match	Length	BB :	a	Description
Н	201	100.0	184	21	AAB08843	Amino acid sequenc
~	201	100.0	184	21	AAY94001	A human BCMA prote
m	201	100.0	184	22	AAE09241	Human BCMA protein
4	201	100.0	184	22	AAE00506	Human B cell matur
2	201	100.0	184	22	AAB60698	Human BAFF recepto
9	201	100.0	184	22	AAY71979	Human B cell matur
7	201	100.0	302	22	AAE00507	Human BCMA-Immunog
۵	201	100.0	302	22	AAB60699	Mouse IqG siqnal/h
6	159.5	79.4	157	22	AAB60700	Human BAFF recepto
10	136	67.7	185	21	AAB08844	Amino acid sequenc
11	136	67.7	185	22	AAY71980	Murine B cell matu

ine ztnf4, lymphocyte	Human 1AC1 spiice Human lymphocyte s Human neutrokine-a	_	Human their protests Human tumour necro	phila	Novel human diagno		Human BR43x2, an i	Drosophila melanog	Drosophila melanog	Pig p105 zona pell			-	Human 5' EST relat	Human reproductive			phila m	c	human	IgG-Fc binding pro	Novel human diagno	Mouse IMC carcinom	Mouse IMC carcinom	Human polypeptide	Human transmembran	Ď,	Novel human diagno
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AAY9	AAW75	AAY94	AAY	ABE	ABG	AAG6	AAY	ABB	ABE	AAN	ABE	ABE	ABG	AAY	AA	AAE	ABG	ABE	ABG	ABG	AAW1	ABG	AAK	AAK	AAO	ABE	ABE	ABG07
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ALIGNMENTS

BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; AAB08843 standard; peptide; 184 AA Amino acid sequence of human. (first entry) 02-JAN-2001 AAB08843; AAB08843 RESULT

Inflammatory response; eptic shock. /note= "putative transmembrane domain" anti-cell death gene; apoptosis; viral infection; rheumatoid arthritis; inflammatory bowel disease; Location/Qualifiers 57...77 Homo sapiens. Domain

24-FEB-2000; 2000WO-US04925. 99US-0121485. WO200050633-A1 24-FEB-1999; 31-AUG-2000

WPI; 2000-558405/51. Seed B, Ting A;

(GEHO) GEN HOSPITAL CORP.

N-PSDB; AAA58559.

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is a necrosis factor (NF) kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; BR43x2; TACI receptor; extracellular domain; BCWA; B cell protein; transmembrane activator and CAWL-interactor; tumour necrosis factor; TNF; activaty; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                                                              The present sequence represents a BCMA (not defined) polypeptide. BCMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 201; DB 21; 100.0%; Pred. No. 3.4e-18;
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                                                                                                         Claim 32; Fig 7A; 53pp; English.
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Matches 34; Conser
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                                                                 expression
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AAY94001
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WPI; 2000-452538/39

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The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor.

TACI is a tumour necrosis factor (TAN) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting taff activity. Eiff 4 is a TYR ligand. They may also be used for inhibiting thing taff activity. Eiff 4 is a TYR ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with a cutoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity asthma, bronchitis, emphysema, end stage renal failure, associated with a stathma, bronchitis, wasculitis, nephritis, pyelonephritis, renal myloidosis, moderating immune response, immunosuppression, graft versus host disease, inflammation, insulin dependent rejection, graft versus host disease, inflammation, insulin dependent collabetes mellitus, Crohn's disease, inflammation, insulin anemala, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, genists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
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TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 184;
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100.0%; Pred. No. 3.4e-18;
ive 0; Mismatches 0;
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                                                                                                              Disclosure; Page 152; 175pp; English.
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2000US-0226986.
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Best Local Similarity 100.
Matches 34; Conservative
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                          The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human
                                               Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or antagonists -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 22;
3.4e-18;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 201; 100.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human B cell maturation protein (BCMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cachero T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE00506 standard; Protein; 184 AA
                                                                                                                                 Example 2; Fig 2; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0157933.
2000US-0181807.
2000US-0215688.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 100.0%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-2000; 2000WO-US27579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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WPI, 2001-541628/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-266242/27
N-PSDB; AAD03844.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              184 AA;
                 N-PSDB; AAD15902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200124811-A1
                                                                                                                                                                                                                                                                                                                                                 BCMA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1999;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE00506;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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associated with undesired call proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRILTR) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL It is also useful for treating autoimmune diseases (Grave's cliseases, systemic lupus srythematosus-SLB); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, communosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.

The present sequence is human APRIL-R also referred as BCMA or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human BAFF-R; BAFF receptor; TWF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell attraction inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour.
                                                                                                                                      The invention relates to a method of treating a mammal for a condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                  proliferation such as cancer or carcinoma, comprisss administering composition comprising A Proliferation Inducing Liband Receptor
  undesired cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ndels
Treating a mammal for a condition associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 201; DB 22;
100.0%; Pred. No. 3.4e-18;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB60698 standard; Protein; 184 AA.
                                                                                               Claim 3; Fig 3A; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BAFF receptor (BAFF-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2000; 2000WO-US22507.
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(APOT-) APOTECH R & D SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                        (APRIL-R) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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treatment of a variety of immune-related disorders. BAFF R is a member of treatment of a variety of immune-related disorders. BAFF R is a member of the TWE (tumour necrosis factor) family, acting as an immunorgulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, PB-cell lymphoproliferative disorders, Mpertension and renal disorders, PB-cell lymphoproliferative cell-induced B-cell growth and menal disorders and HIV in the treatment of immunosuppressive disorders and HIV in the BAFF-R proteins or BAFF-R proteins or BAFF-R protein an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases cuch as systemic lupus erythematosus, autoimmune haemolytic anaemia, replidly progressive disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive growth and maturations. Since BAFF-R progressive glomerulonephilitis, and lymphomas. Nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; hamenlytic anaemia; Grawe's disease; myasthenia gravis; chromosome 16; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                                                                                                                                                                                         The invention relates to the use of a BAFF receptor (BAFF-R, also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rhematoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus:
                                                                                                                                            Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell Jympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents human BAFF-R.
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Ambrose C, Tschopp J, Schneider P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 201; DB 22;
100.0%; Pred. No. 3.4e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human B cell maturation factor (BCMA) protein.
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                                                                                                                                                                                                                                                                      Claim 20; Fig 1; 59pp; English.
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Best Local Similarity 100.
Matches 34; Conservative
     Browning J,
                                                                       WPI; 2001-202866/20
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                                                                                                N-PSDB; AAF59998
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                      Thompson J;
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1..02 /label= Extracellular_domain

Location/Qualifiers

Homo sapiens

Key ∱ Domain

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                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Tumour necrosis factor (TNF) and ApoL-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, coodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; Immunosuppressive disease;
                                                                                                                                                                                                                                                                                                  Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kidney, pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte
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3.4e-18;
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                                                                                                                                                                                                                                                                                                                                                                            Claim 37; Page 104-105; 112pp; English.
                                                                                                                                                                      (NAJE-) NAT JEWISH MEDICAL & RES CENT
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                                                                        05-MAY-2000; 2000WO-US12266
                                                                                                                             01-MAY-2000; 2000US-0201012
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                                                                                                                                                                                                                                             WPI; 2001-016094/02.
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WO200068378-A1.
                                                                                                             06-MAY-1999;
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protein, BAFF-R-Fc.

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carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and
orgån transplantation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMA; fusion protein; immunoglobulin G; IgG; Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCN or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also referred as BCMA or BCM protein, Fc region of human immunoglobulin G (IgG) and a signal sequence from murine Ig kappa cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is a fusion construct containing human APRIL-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comparising A Proliferation Inducing Ligand Receptor ARPET. P. artaconist
                                                                                                                                                          /label= Signal_peptide
/note= "Derived from murine Ig kappa sequence"
                                                                                                                                                                                                                                                                                                                    /label= Cysteine_rich_domain
/note= "Derived from human BCMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cachero T,
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 3B; 85pp; English.
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/label= (
                                                                                                                                                                                                                                                                   ..302
                                                                   Chimeric - Homo sapiens.
Chimeric - Mus sp.
                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APRIL-R) antagonist
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N-PSDB; AAD03847.
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                                                                                                                                             Protein
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                                                                                                                                                                                                                                   Region
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Best Local Similarity

Matches

Query Match

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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders BAFF-R is a member of the TNR (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendrition, and in the treatment of autoimmune disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative disorders, and in patients undergoing organ transplantation. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating.

Cupic and in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. Since BAFF-R specific antibodies may be used for treating diseases such as systemic lupus erythematosus, autoimmune hammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune hammaia, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                  Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; be-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; autoimmune haemolytic anaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; IGG FC; fublon construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider P;
                                                                                                                                                                                                                                                                                          Mouse IgG signal/human BAFF-R/human IgG Fc fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Browning J, Ambrose C, Tschopp J,
                       31 csqneyfdsllhacipcqlrcssntppltcqryc 64
1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                      AAB60699 standard; Protein; 302
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11-FEB-2000; 2000US-0181684.
18-FEB-2000; 2000US-0183536.
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                                                                                                                                                                                                                                             22-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
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N-PSDB; AAF59999.
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/label= Mature_human_BCMA_IgG_Fc_fusion_protein
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                                                                                                                                                                                                                                                                                                                                                         "Derived from human IgG Fc region"
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                                                                                                                                                                                                                                                                                                            "Derived from human BCMA protein"
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1 Similarity 100.0%; Pred. No. 5.6e-18;
34; Conservative 0; Mismatches 0;
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cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, between BAFF-R specific antibodies may be used for treating pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematchous, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephitis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
                                                                                                                                                                                                                                                                                 present sequence represents a human BAFF-R protein sequence as encoded by plasmid PJST535. However, this BAFF-R protein sequence is 27 amino acids shorter than that given in AAB60698.
                                                                                                                                                                                                                                                                                                                                                                  157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immune related disorder; B.cell growth inhibitor; BCMA;
B-cell maturation inhibitor; immunoglobulin production inhibitor;
autoimmune disorder; b-cell lymphoproliferative disorder; hypertension;
renal disorder; immunosuppressive disorder; HIV infection;
organ transplantation; antiinflammatory; systemic lupus erythematosus;
autoimmune haemolytic anaemia; Grave's diseases, multiple myeloma;
B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
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human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-FC, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human BAFF-R and a human IgG Fc sequence.
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor (BAFF-R) sequence encoded by A plasmid pJST535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
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                                                                                                                                                                                Length 302;
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                Score 201; DB 22;
Pred. No. 5.6e-18;
; Mismatches 0;
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                                                                                                                                                                                                                                                               1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                     csqueyfdsllhacipcqlrcssntppltcqryc 64
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11-FEB-2000; 2000US-0181684.
18-FEB-2000; 2000US-0183536.
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(APOT-) APOTECH R & D SA.
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N-PSDB; AAF60000.
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Best Local Similarity
                                                                                                                      302 AA;
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Thompson J;
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AAB6070
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                                                                                                                                                                                                                                                     BCMA, necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is
                            Gaps
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 Length 157;
                          Indels
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 DB 22;
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79.4%; Score 159.5; DB 2 90.6%; Pred. No. 6.2e-13;
                                                                                                                                                                                                                              Amino acid sequence of murine BCMA polypeptide.
              Pred. No. 6.2
0; Mismatches
                                                    3 QNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                   Location/Qualifiers
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                                                                                                                                                 AAB08844 standard; peptide; 185
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                                                                                                                                                                                                   (first entry)
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                          Conservative
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              Similarity
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1;
            activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine, Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenta purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; BCAA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation; post-streptococcal glomerulonephritis; polyarteritis nodosa.
to identify compounds which modulate BCMA activity (and thus NF-kB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to Tumour necrosis factor (TNF) and ApoL-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The
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                                                                                                                                                                                                                                                                                                Length 185;
                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 7.6e-10;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine B cell maturation factor (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                 Claim 37; Page 107-108; 112pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY71980 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                67.7%;
70.6%;
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                                                                                                                                                                                                                                              185 AA;
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                                                                                                                                                                                                                  designing.
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invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid trathitis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune hemenlytic anaemia, autoimmune thrombocytcopenia purpura, goodpasture's syndrome, pemphigus vulgaris, acute iheumatic fever, post-streptococcal glomerulonephiritis, or polyarteritis nodosa.

The TALL-1 protein and its corresponding nucleic adid sequence are also useful in diagnostic assays.

The present sequence is a murine B cell maturation factor (BCMA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAMI-interactor; tumour necrosis factor; TNF; actif4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclarosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anneamis; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 136; DB 22;
Pred. No. 7.6e-10;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A murine ztnf4, a tumour necrosis factor ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yee DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY94006 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                 67.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-2000; 2000WO-US00396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0226533,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gross JA, Xu W, Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.7
Best Local Similarity 70.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-452538/39.
                                                                                                                                                                                                                                                                                                                                                              185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA58566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200040716-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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         The present sequence represents murine ztnf4, a tumour necrosis factor ligand. The extracellular domains of BR4x2 (an isoform of the transmembrane activator and CAM-interactor (FTCI) receptor). TACI or ECCE CKMA (a related B cell protein) contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. They may also be used for and are inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with an autoimmune disease selected from systemic lupus erythematosus, myasthenia cutoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The zinf4 activity and BR4x2, TACI or BCMA receptor-ligand engagement is associated with asthma. bronchitis, emphysema, end stage renal failure, capture, asthma, bronchitis, emphysema, end stage renal failure, capture, and untiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft crejection, graft versus host disease, inflammation, insulin dependent crejection, graft versus host disease, inflammation, insulin dependent septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery construction, or occlusion, and cholesterol or renal emboli.
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                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium signal-modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B-cell; B lymphocyte; laffection. cancer; rheumatoid arthritis; autoimmune disease; glomerulonephitis; immunosuppressive; graft versus host disease; transplant rejection; therapy; signal transduction.
                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated transmembrane activator protein - used to develop
                                                                                                                                                                                                                                                                                                                                   DB 21; Length 249;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lymphocyte surface receptor extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane activator and CAML-interactor;
                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                Score 71.5; Di
Pred. No. 0.2;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    6 cpkdqywdssrkscvscaltcsqrs-qrtctdfc 38
                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW75785 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 73; 89pp; English
                                                                                                                                                                                                                                                                                                                                 35.6%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0810572.
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                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bram RJ, Von Bulow G;
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                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                          249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV57330.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW75785;
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW75785
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extracellular, domain of novel human transmembrane activator and catterior catterior. CaML-interactor (TACI) protein (see AAW15783). TACI is a lymphocyte receptor protein that is involved in the calcium activation pathway. It is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. The extracellular domain of TACI functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the C-terminal portion (see AAW15784) of TACI to the N-terminal domain of CAML. A recombinant form of the extracellular portion of TACI acts as a dominant-negative or extracellular portion of TACI acts as a dominant-negative or used to treat or prevent autoimmune disease, graft rejection or used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TACI, in which binding of a candidate molecule is determined by detecting cellular activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marsters SA, Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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the amino acid sequence of the N-terminal, i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%; Score 66.5; DB
32.4%; Pred. No. 0.57;
tive 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : |: | | |: |: |: |: || :| |: || :| |: || :| || 34 cpeeqywdpllgtcmsckticnhqs-qrtcaafc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE09244 standard; Protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TACI splice variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 6; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-2000; 2000WO-US32378.
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22-AUG-2000; 2000US-0226986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.1
Best Local Similarity 32.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashkenazi AJ, Dodge KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200160397-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-2001
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AAE09244
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                 antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL and Expression or activity. TALL-1 and APRIL and TALL-1 with TACI or BLOCK the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psociasis and lupus erythematosus. The present sequence is human
The invention relates to methods of using one or more agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACI; transmembrane activator and CAML-interactor; calcium signal-modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B-cell; B lymphocyte; infection; cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis; immunosuppressive; graft versus host disease; transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and
                                                                                                                                                                                                                                         Length 265;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                           DB 22;
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/label= Extracellular_domain
/note= "Claim 8"
                                                                                                                                                                                                                                         Score 66.5; DB Pred. No. 0.92; B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                  187..294
/label= Cytoplasmic_domain
/note= "Claim 6"
                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lymphocyte surface receptor TACI.
                                                                                                                                                                                                                                                                                                                                                                                                       AAW75783 standard; Protein; 293 AA
                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                         33.18;
                                                                                                                                                                  TACI splice variant protein.
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                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bram RJ, Von Bulow G;
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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N-PSDB; AAV57328.
                                                                                                                                                                                               265 AA;
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                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW75783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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activator and CAML-interactor (TAGI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TAGI is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to Specifically regulate B cell responses without affecting T cell activity. TAGI CDNA (seev57328) was isolated from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also claimed are cDNA library using a yeast two-hybrid assay. Also claimed are attribodies to TAGI protein. Methods are claimed for identifying a mitubodies to TAGI protein. Methods are claimed for identifying a mature T lymphocytes. TAGI can be activated to increase immune control to provide immunosuppressive for treating activity, e.g. for treating infections or carders. It can be blocked to provide immunosuppression, e.g. for treating autoimmune and inflammatory conditions such as immune complexinduced vasculitis, space induced vasculitis, space increase immore complexind activity and hyperacute xenograft rejection, rheumatoid arthritis, experimental allergic and hyperacute xenograft rejection, rheumatoid arthritis, experiment or systemic lupus erythemmetosus, transplant rejection, cannot or control or con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 293;
                                                                                                                                                                   This is the amino acid sequence of novel human transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
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Pred. No. 1;
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                                                                                                  Claim 20; Fig 2a; 89pp; English.
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32.4%;
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Best Local Similarity 32.4
Matches 11; Conservative
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US-09-249-451-7 US-08-809-455-7 US-09-249-471-7 US-09-249-472-7

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US-09-249-451-40
US-08-809-455-4
US-08-809-455-4
US-09-249-461-4
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US-09-249-48-40
US-09-249-48-40
US-08-465-380-7
US-08-480-399-7
US-08-480-399-7
US-08-480-399-7
US-08-480-395-7

Sequence Sequence

Sequence

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APPLICANT: Bram, Richard J.
APPLICANT: Worm Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 26,742
RELECOMMUNICATION INFORMATION:
TELEPONE: 201-487-5800
TELEPAX: 201-487-5800
FORMATION FOR COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
                                                                                                                                                                                                                                Sequence 6, Application US/08810572A Patent No. 5969102 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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ORIGINAL SOURCE:
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STATE:
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June 25, 2002, 16:12:12; Search time 35.41 Seconds (without alignments) 23.453 Million cell updates/sec
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Sequence 4, Appli
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Sequence 2,
Sequence 9,
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Sequence 1.
Sequence 4.
Sequence 4.
Sequence 3.
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Sequence 2
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Sequence 3
Sequence 4
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                                                                                                                                                                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                  1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
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US-09-290-333-2
US-09-257-580-2
US-08-718-388-9
US-08-718-388-9
US-08-117-080-12
US-08-45-380-4
US-08-465-380-4
US-08-465-380-4
US-08-466-399-4
US-08-466-399-40
US-08-466-399-40
US-08-461-965-4
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Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Length 166;

DB 2;

Score 66.5;

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ARD INFORMATION.
APPLICANT: Brain, Richard J.
VON BULOW, GOTZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
      APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A FILING DATE: US/08/8110N: US/08/8110N: US/08/8110N: TELEPRANTION: TELEPRANTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-345 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: SEQUENCE 293 amino acids
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32.4%;
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COUNTRY: USA
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STATE: New Jersey
COUNTRY: USA
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Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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Best Local Similarity 32.4%; Pred. No. 0.43;
Matches 11; Conservative 8; Mismatches
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32.4%; Pred. No. 0.43;
Live 8; Mismatches
                                                                                             1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                    | : :|:| | | : |: | : | : | : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <a href="https://doi.org/10.10/10/10/10/10/">doi: org/10/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 166 amino acids TYPE: amino acid
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0uery Match
Best Local Similarity 32.48
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-810-572A-2
                                                                                                                                                                                                                                                                               US-09-290-333-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-290-333-6
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Patent No. 6271362

GENERAL INFORMATION:
APPLICANT: MORITAWA, MINORU
APPLICANT: HARADA, NAOKI
TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 381;
                                                                                                                                                                                            Score 56; DB 2; Length 2476;
Pred. No. 1e+02;
                                                                                                                                                                                                                                     ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,388 FILING DATE:
                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                Score 53.5; DB 4;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                          1 CSQNEYFDSLLHACIP-CQ---LRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yorkshire Cancer Research
TITLE OF INVENTION: Tumour Suppressor Gene
FILE REFERENCE: Canine p53
CURRENT APPLICATION NUMBER: U$/09/257,580
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 9804178.3
PRIOR FILING DATE: 1998-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 NEYFDSLLHACIPCQLRCSSNTPPLTCQR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-257-580-2; Sequence 2, Application US/09257580; Patent No. 6307036; GENERAL INFORMATION:
                                                                                                                                                                                       Query Match 27.9%;
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.69
Best Local Similarity 48.33
Matches 14; Conservative
    SEQUENCE CHARACTERISTICS
                                                                                                , MOLECULE TYPE: protein US-08-276-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VA
COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Canis
US-09-257-580-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
LENGTH: 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-718-388-9
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APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
WUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
                                                                                                FILING DATE: 12-Apr-1999
CLASSIFICATION: CURRICOWN>
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET UNDHER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR ESQ ID NO: 2:
SEQUENCE CHARACTER/STICS:
LENGTH: 293 amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66.5; DB 4;
Pred. No. 0.74;
8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : | : | | | : | : | : | : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                APPLICATION NUMBER: US/09/290,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UISD:418\KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOSEE: Arnold, White & Durkee Tr. P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 33.18;
1 Similarity 32.4%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-290-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
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Gaps
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                                                                                                                                                                      25.6%; Score 51.5; DB 1; Length 63; 38.5%; Pred. No. 9.9; tive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST STREET: TOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                             ; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2 US-08-117-080-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2 US-08-471-329-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROBKAERT, WILLEM F
APPLICANT: CAMME, BRUNO PA
APPLICANT: CAMME, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESSED: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%; Score 51.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT AFFLICATION NUMBER: US/08/471,329
FILING DATE: 02-JUN-1995
CLASSIPTECATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,080
FILING DATE: 10-MAR-1997
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1997
FILING DATE: 11-MAR-1991
                                                                                                                                                                                                                                                                10 LLHACIPCOLRCSSNT-PPLTCORYC 34
                                                                                                                                                                                                                                                                                            24 MIEACIGNGGRCNENVGPPYCCSGFC 49
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08471329
Patent No. 5689048
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                Best Local Similarity 38.5
Matches 10; Conservative
                                   MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-471-329-12
                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.6%; Score 53.5; DB 4; Length 5405; Best Local Similarity 34.3%; Pred. No. 4.3e+02; Matches 12; Conservative 5; Mismatches 13; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08117080
Patent No. 548298
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 2733 CPQNSHXE----LCADTCSLGCSALSAPLQCPDGC 2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSQNEYFDSLLHACI-PCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELERAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENTH: 63 amino acids
                                                                                                   0230-111
CLASSIFICATION: 536
ATTORREY/AGENT INFORMATION:
NAME: WURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-718-388-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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US-08-117-080-12
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Length 77;
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                                                                                          Sequence 4, Application US/08465380

Patent No. 5863894
GENERAL INFORMATION:
GEORGE P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Perer W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-465-380-40
Sequence 40, Application US/08465380
Sequence No. 2863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yes R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%; Score 51.5; 1
29.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: SUCRED COMPUTER: SUCRED COMPUTER: IBM COMPUTER: SUCRED COMPUTER: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/465,380 FILING DATE: June 5, 1995 CLASSIFICATION: 530 PRIOR APPLICATION NUMBER: 08/326,110 FILING DATE: October 18, 1994 ATTORNEY/AGENT INFORMATION: NAME: BIGGS, SUZANNE L. REGISTATION NUMBER: 30,158 REFERENCE/DOCKET NUMBER: 213/268 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Ancyclostoma caninum US-08-465-380-4
                                                                                                                                                                                                                                                                                                                                                    E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Thes 12; Conserva
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TOPOLOGY:
                                                                            US-08-465-380-4
                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                     Gaps
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                                                                                                                                                                                                              Sequence 12, Application US/08915142
Patent No. 594263
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUND PA
APPLICANT: CAMMUE, BRUND PA
APPLICANT: REES, SARAH B
ITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/915,142
FILING DATE: 800-0404-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
             Pred. No. 9.9;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 20-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,329
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/17,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA: 1992
PRIOR APPLICATION DATA: 1991
PRIOR APPLICATION DATA: 1991
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELEFAX: (202) 861 3000
TELEFAX: 67146.2 CUSH
INFORMATION FOR SED ID NO: 12:
                                                                                                     24 MIEACIGNGGRCNENVGPPYCCSGFC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LLHACIPCQLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLHACIPCQLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.6%;
38.5%;
          38.5%;
Best Local Similarity 38.5%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.59
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA ZIP: 20005-3918 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
                                                                                                                                                                                               US-08-915-142-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-915-142-12
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.6%; Score 51.5; DB 2; Length 77 Best Local Similarity 29.3%; Pred. No. 12; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08486397

Sequence 4, Application US/08486397

Patent No. 586542

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Larcohe, Laurent S. Jespers, APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 631 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICKSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-UUN-1995
CLASSIFICATION DATA:
APPLICATION UNMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELECOMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
THE COMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORT Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
(213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
       California
                                  U.S.A.
                                                         90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-480-478-33
                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-486-397-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
MUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CGENEWLDD----CGTQKPCEAKCNEEPPEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSONEYFDSLLHAC --- IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
TITLE OF INVENTION: COAGULANT PROTEIN
NUMBER OF SOUGHNES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.6%; Score 51.5; DB Best Local Similarity 29.3%; Pred. No. 12; Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GEORGE P. VLASUK; PATRICK ERIC APPLICANT: HUGO STANSSENS; JORIS HILDA APPLICANT: LIEVEN MESSENS; MARC JOZEF APPLICANT: LAUWEREYS; VVES RENE LAROCHE; APPLICANT: LAUWEREYS; VVES RENE LAROCHE; APPLICANT: YANNICK GEORGES JOZEF APPLICANT: GANSEMANS
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFCATION TOWN:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFCATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY, AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/08480478
Patent No. 5864009
GENERALIREORMATION:
APPLICANT: GEORGE P. VLASUK; PATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...owESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los bar-1
                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
SY: linear
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US-08-480-478-33
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Indels 11; Gaps
                                                                                                                                                                                                                                                                    Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 25, 2002, 16:12:12
Job time: 52 sec
                                                                                                 ; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
ORGANISM: Ancyclostoma caninum
US-08-486-397-40
                                          : 77 amino acids amino acid
                  SEQUENCE CHARACTERISTICS:
                                                                                              linear
                                                                 TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 40, Application US/08486397
| Patent No. 5866542
| GENERAL INFORMATION:
| APPLICANT: George P. Vlasuk, Patric H. Stanssens,
| APPLICANT: George P. Vlasuk, Patric H. Stanssens,
| APPLICANT: Yors R. Laroche, Laurent S. Jespers,
| APPLICANT: Year R. Laroche, Laurent S. Jespers,
| APPLICANT: Year B. Laroche, Laurent S. Jespers,
| APPLICANT: Year B. Bergum
| TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT;
| TITLE OF INVENTION: PROTEIN
| NUMBER OF SEQUENCES:
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.6%; Score 51.5; D
Best Local Similarity 29.3%; Pred. No. 12;
Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: Diskette, 1.44 Mb
PEDIUM TYPE: Storage
COMPUTER: Diskette, 1.44 Mb
PEDIUM TYPE: Storage
COMPUTER: Diskette, 1.44 Mb
PEDIUM TOWNER: US/08/486,397
FILING DATE: JUNE 5, 1995
CLASSIFICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATYGNEY FACENT INFORMATION:
NAME: BIGGS, SUZARNE L.
REGISTRATION NUMBER: 30,156
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE I.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEXX: (7-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90071
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 25, 2002, 16:13:22; Search time 52.94 Seconds (without alignments) 301.300 Million cell updates/sec Run on:

US-09-854-864-15 909 1 MSGLGRSRRGGRSRVDQEER.....SPALPGLKLSADQVALVYST 166

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ŋ	, Description	serine proteinase	cathepsin B-like c	furin (EC 3.4.21.7		mucin, submaxillar	subtilisin-like pr		PACE4A - mouse (fr	_	gp330 protein prec	protein-tyrosine-p	protein-tyrosine k	gene PACE4 protein	hypothetical prote	hypothetical prote	apolipoprotein E r	probable vitelloge	molybdopterin oxid	estrogen-responsiv	laminin B1k chain	variant-specific s	hypothetical prote		2	probable iron-sulf	hypothetical prote	cartilage intermed	furin (EC 3.4.21.7	,
SUMMAKIES	ID	534583	T06466	T43251	AD0299	T03099	G02428	JC6148	152527	S53457	T42737	JH0609	I58388	153282	H69834	T25169	JE0237	T13171	C69312	A49656	A53612	A45664	T19364	T34264	A55624	AF0273	T15230	T09484	A43434	370177
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	Length	1548	353	1299	355	13288	899	915	932	1650	4660	773	1124	937	108	330	966	1984	269	630	1170	296	230	2195	2871	620	751	1184	1680	1073
ď	Query Match	10.7	9.5	9.5	9.3	9.1	9.1	9.1	9.0	9.0	9.0	8.9	8.9	8.9	8.8	8.8	8.8	8.7	8.7	8.6	8.6	9.8	8.5	8.5	8.5	8.5	8.5	8.5	8.4	α
	Score	97.5	86.5	98	84.5	83	82.5	82.5	82	82	82	81	81	80.5	80	80	80	79.5	79	78.5	78.5	78	77.5	77.5	77.5	77	77	77	76.5	76.5
	Result No.	1	7	m	4	S	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	00

dnaJ-like protein protein protein B024.8 [i probable proprotein cnib protein - Tet hypothetical prote hypothetical prote subtilisin-like protein protein listin-like protein libnarogolobu alpha-2-macroglobu protein-tyrosine-protein-tyrosine-protein-tyrosine-protein-tyrosine-protein-lintegrin su	_change 05-Nov-1999 large Cys-rich region of PC6, 7.1; PID:d1005033; PID:g44037	ngth 1548; ndels 23; Gaps 7;HQSQRTCAAF 65	ne All6) - wheat (fragment) t_change 11-May-2000 equence homology to cathepsin equence homology to cathepsin oots nce)
145812 B88465 B88465 B88465 S42136 S38032 JG5571 A39490 A7321 A39490 A47221 A47221 S48748 I61512	ALIGNMENTS) PC6B - mouse se mouse) .e.revision 10-Nov-1995 #text .i. Nakayama, Ki. isoform with an extremely langle; 93327934 MUID: 93327934 .i. NID: 9407344; PIDN: BAA04567	e 97.5; DB 2; Le ismatches 32; I he le	se (EC 3.4.22) (clo bn wheat) sion 23-Apr-1999 #tex . C.; Baulcombe, D.C. ane from wheat with s 1258430 from GB/EMBL/DDBJ From GB/EMBL/DDBJ From GB/EMBL/DDBJ Priggl698; PIDN:CAA46 Spring, etiolated sh red (incomplete seque
367 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	(EC 3.4.21) PC6B culus (house mouse) sequence_revision as action of an isoform ation of an isoform ation of an isoform ary RNA cult.	10.7%; Scor Conservative 12; M ERFPQGLWTGVAMRSCPEGOY ERFLYHGECLENCEVGHY -CRSLSCRKEQGKFYDHLLRD 	protein vum (com lence_rev lence_rev lence_rev lence l
œœœœœœœœœœœœ 44 44üüüüüüüüüüüüü	1 rocteinase (EC 3.4.21 s: Mus musculus (house 02-bec-1933 #sequence. ion: S34583 identification of an ince number: S34583; Mu ince system man ince number: S34583; Mu ince type: mRA is preliminary ile type: mRA references: GB:D17583; des: 1-1548 «NAA references: GB:D17583;		n B-like cysteine 23. Triticum aestiv 23. Apr-1999 #seque ion: T06466 2, F.J.; Murphy, G., 2, 9.37-948, 1992 A gibberellin-reg noce number: 215659 ion: T06466 : preliminary; tra preliminary; tra le type: DNA es: 1-353 <cej> references: EMBL:X mental source: Cv. cor. ion: intro positions n amily: papain ds: cysteine prote</cej>
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	proteinase les: Mus mus 02-bec-19 ssion: S345 saion: S345 stt. 327; M stt. 37; I dentifi- ence numbe ssion: S345 ssi prelimi- vule type: vule t	n O	RESULT 2 T06466 cathepsin B-like cy. Cipecies 13-pt-1999 CiAccession: T06466 Riceludo, F.J.; Mur; Rejudo, F.J.; Mur; Riceludo, F.J.; Mur; Riceludo, F.J.; Mur; Riceludo, F.J.; Mur; A; Reference number: A; Reference number: A; Reference number: A; Rolecule type: DN A; Rolecule type: DN A; Rolecule type: DN A; Rolecule type: DN A; Rosidues: 1-353 </td
W H W W W W W W W A A A A A A A A A A A	RESULT 1 S34583 serine proteinase (EC 3.4.21) C; Species: Mus musculus (house. C; Date: 02-Dec-1993 #sequence_r. C; Accession: S34583 R; Nakagawa, T.; Murakami, K.; N FEBS Lett. 327, 165-171, 1993 A; Title: Identffication of an i A; Reference number: S34583; MUI A; Accession: S34583 A; Status: preliminary A; Molecule type: mRAA A; Residues: 1-1548 na.hydrolase ; Serine p C; Keywords: hydrolase; serine p	Query M Best Lo Matches Qy 14 Db 627 Qy 66	RESULT 2 T06466 Cathepsin B- C.Species: T2- C.Date: 23-An C.Accession: R.Cejudo, F., Plant J. 2, A.Title: A g A.Reference A.Reference A.Reference A.Reference A.Residues: A.Residues: A.Cross reservations A.Residues: A.Residues: A.Residues: A.Residues: A.Residues: C.Genetics: C.Genetics: C.Superfamil

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A, Cross-references: GB: AL590842; PIDN: CAC91256.1; PID: 915980445; GSPDB: GN00175
                                  C;Genetics:
A;Gene: YPO2451
C;Superfamily: Escherichia coli yceA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1572-1607 < EC2>
C; Superfamily: pig submaxillary mucin
C; Keywords: tandem repeat
                                                                                                                                                                                                                                                           al Similarity 24.49
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 furin (EC 3.4.21.75) - fall armyworm
NyAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C;Species: Spoodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43251
R;Cieplik, M; Klenk, H.
submitted to the EMBL Data Library, January 1996
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A;Recession: T43251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recelectic enumber: 223368
A;Accession: T43251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1299 <CIE>
A;Cross-references: EMBL:268888; NID:g1167859; PID:e219690; PIDN:CAA93116.1
A;Experimental source: clone Sfurin 6; ovary
C;Function:
A;Description: responsible for the endoproteolytic processing of proproteins with specif
C;Keywords: hydrolase; serine proteinase
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(Species: Yersinia pestis

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-----PE----NGECI 1192
                                                                                                                                                                                                                                73 KEQGKFYDHL-----LRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRRQRSGE 125
                                                                                                                                                                                                                                                                                                                                                                                     133 ALQDRFCIHLNMSVSLSVNDLLAC------CGFLCGSGCNGGYPISAWRYFRRSGV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 -----YDHLLRDCISCASICG----QHPKQCAYFCENKLRSPVNLPPELRRQRSGEVE 127
                                                                                                                                                                                   22 POGLWTGVAMRSCPE------EQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                         Length 353;
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                                                                                                              Indels
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                                                                                                          63;
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                                      DB
                                  ; Score 86.5; DE; Pred. No. 2.7; 12; Mismatches
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                                                                                                          Conservative
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A;Molecule type: DNA
A;Residues: 1-355 <KUR>
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Mucin, submaxillary - pig

N.Alternate names: apomucin
C.Species: Sus acrorfa domestic pig)
C.Species: Sus acrorfa domestic pig)
C.Species: Sus acrorfa domestic no. 24-Mar-1999 #text_change 02-Jun-2000
C.Saccession: T03099; A40009; A28528; B29789
R.Schardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNA sequence and structural polymorphism of the polypeptide chances in the complete cDNA sequence and structural polymorphism of the polypeptide chances in preliminary; translated from GB/EMBL/DDBJ
A;Residuas: preliminary; translated from GB/EMBL/DDBJ
A;Residuas: 1-1388 &ECX>
A;Cross-references: EMBL:AR065273; NID:92581863; PIDN:AAC62527.1; PID:92581864
B;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
J. Biol. Chem. 266, 9678-9686, 1991
A;Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain A;Reference number: A40009; MUID:91236743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 12139-12167, T',12169-13288 <EC3>
A; Residues: 12139-12167, T',12169-13288 <EC3>
A; Cross-references: GBH661883; NID:9454837; PIDN:AAA30998.1; PID:9164374
A; Cross-references: GBH61883; NID:9454837; PIDN:AAA30998.1; PID:9164374
B; Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988
A; Title: Porclaine submaxillary gland apomucin contains tandemly repeated, identical se A; Accession: A28528; MUID:88087170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr., W.C.; Hill J. Biol. Chem. 262, 11339-11344, 1987
A;Title: Structural properties of porcine submaxillary gland apomucin.
A;Reference number: A92606; MUID:87280230
A;Accession: B29789
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A;Rosidues: 12139-12167, 'T',12169-12641 <TIM>
A;Cross-references: GB:M21174; GB:U03512; NID:9164321; PIDN:AAA30990.1; PID:9552360
A;Experimental source: submaxillary gland
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                                                                                                                                                                                                                                                                    257 ERISDDVIAHCHQCGTPCDAHTN-----CKNDGC------HLL--FIQCPVCAAKF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                         300 EGCCSQICQEELK----LPQEEQRSRRAGRENGIKIFNKSKGL----LQATMHIPSPEKS 351
                                                                                                                                                                             37 EQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQH 96
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Length 355;
                                                                                           48; Indels
         5,
         <u>B</u>
9.3%; Score 84.5; D
24.4%; Pred. No. 4;
tive 20; Mismatches
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Db 13075 EEKSPGDVWTANCHKCTCTEAKTVDCKPKECPSPPTCKTGERLIKFKANDTCCEIGH 13131 Qy 71 CRK	27 719 72
RESULT 6 G024218 subtilisin-like proprotein convertase (EC 3.4.21) 5 precursor - human (fragment) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: G02428 R; Reudelhuber, T.L. submitted to the EMBL Data Library, February 1996 A; Reference number: H01242 A; Reference number: H01242 A; Reference number: H01242 A; Rocession: G02428 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Rocious: Lype: mRNA A; Residues: 1-899 < REU> A; Residues: 1-899 < REU> A; Residues: 1-899 < REU> A; Cooss-references: EMBL: U49114; NID: g1218057; PIDN: AAA91807.1; PID: g1218058	RESULT 8 ISESULT 8 ISESULT 8 ISESULT 8 ACCE4A - mouse (fragment) C;Species: Mus musculus (house mouse) C;Accession: 152527 R;Hosaka, M.; Murakami, K.; Nakayama, K. Biomed. Res. 15, 383-390, 1994 A;Title: PACE4A is a ubiquitous endoprotease that has similar but not identical subst A;Reference number: 152527 A;Accession: 152527 A;Accession: 152527 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-932 < RES. A;Residues: 1-932 < RES. A;Cross-references: GB:D50060; NID:9769700; PIDN:BAA08777.1; PID:9769701 C;Superfamily: subtilisin-like proteinase PACE4; subtiliain homology
Superfamily: subtilisin-like proteinase PA Keywords: hydrolase; serine proteinase 148-386/Domain: subtilisin homology <sbt></sbt>	P:11/2-#10/Domain: Subilisin nomology <sbt> Query Match Query Match Best Local Similarity 25.0%; Pred. No. 15; Matches 28; Conservative 16; Mismatches 44; Indels 24; Gaps 5; Oy 16 DQEERFPQGLWTGYAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCRK 73</sbt>
vati WDPI DDTK	: :: :: :: ::
QY 72 RKEQGKFYDHLLRDCISCASICGQHPKQCAVFCEN 106 1 1::::	RESULT 9 S53457 dominant autoantigen ap 330 - rat (fragment)
	'sregicus (Norw'sequence_revi lanikov, A.V.; 713, 1995 1916cular forms 53457; MUD:9
A; Reference number: JC6148; MUID:96353880 A; Contents: CEM T-cell A; Contents: CEM T-cell A; Accession: JC6148 A; Molecule type: mRNA A; Residues: 1-915 < MINA A; Residues: 1-915 < MINA A; Consorreferences: GB:U56387; NID:91498312; PIDN:AAC50643.1; PID:91498313 C; Comment: This protein functions as a soluble enzyme within the secretory pathway. It is	TOK> 2-macrogleceptor lreceptor homology homology receptor receptor receptor
Cydenetics: A;Gene: pc6A C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C;Keywords: glycoprotein; hydrolase; serine proteinase C;Keywords: glycoprotein; hydrolase; serine proteinase F;164-402/Domain: subtilisin homology <sbt> P;164-402/Domain: subtilisin homology <sbt> Query Match Query Match 9.1%; Score 82.5; DB 2; Length 915; Best Local Similarity 26.0%; Pred. No. 14; Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;</sbt></sbt>	

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A; Accession: PS0366
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 88-91, KY, 94-109, LA', 112-118, 'S', 120-122 <DE4>
A; Experimental source: embryonic carcinoma cell, P19 cell, clone PTP42
Blood 78, 2222-2228, 1991
A; Ti, Li, Eleveland, J.L. Ihle, J.N.
Blood 78, 2222-2228, 1991
A; Reference number: A61180; MUID:92032882
A; Accession: G61180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Status: not compared with conceptual translation
A. Molecule type: mRNA
A. Residues: 124-127, '1',129-229 < VIA>
C. Comment: This protein is a located in the cytoplasm.
C. Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosphatase catalytic domain #status predicted < PCD>
F. S29/Domain: protein-tyrosine-phosphatase homology < PPP>
F. S23. Active site: Cys (phosphocysteine inferemediate) #status predicted
F. 231. Active site: substrate phosphate (Arg) #status predicted
                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
S;Accession: JH0609; PS03165; PS03166; G61180
R;Accession: JH0609; PS03165; PS03166; G61180
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A;Titte: Differential expression of a novel murine non-receptor protein tyrosine phos A;Reference number: JH0609; MUID:92272714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - human C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C; Accession: 158388
R; Ziegler, S.F.; Bird, T.A.; Schneringer, J.A.; Schooley, K.A.; Baum, P.R. Oncogene 8, 663-670, 1993
A; Title: Molecular cloning and characterization of a novel receptor protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:CAA45037.1; PID:9416182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 PVNLPPELRRQRSGEVE--------NASDNSGRYQGLEHRGSEASPALP 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. Accession: PS0365
A. Status: nucleic acid sequence not shown
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Accession: PS0369
A. Accession: PS0369
A. Accession: PS0369
A. Status: nucleic acid sequence not shown
A. Molecule type: mRNA
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A. Residues: B8-91, 'G', 93-109, 'LG', 112-120, 'T', 122 < DE3>
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A. Residues: B8-91, 'G', 93-109, 'T', 120 < DE3>
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-773 <DEN>
A;Cross-references: GB:X63440; GB:S36169; NID:9416181; PII
A;Experimental source: embryonic carcinoma cell, P19 cell
                                           protein-tyrosine-phosphatase (EC 3.1.3.48) P19 - mouse N.Alternate names: protein-tyrosine-phosphatase PTPTY43
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Best Local Similarity
Matches 45; Conserv
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A) Residues: 1-4660 (SAI>
A) Cassareferences: EMBL:L34049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A) Experimental source: strain Sprague-Dawley; kidney
C) Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-4660/Product: gp330 protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                         #status atypical <YW08>
#status atypical <YW09>
<YW10>
                                                                                                                                                                                                                                                                          <YW07>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 11-3m-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42737
R;Saito, A.; Pletromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of A;Reference number: A58173; MuID:95024033
A;Accession: T42737
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4660 <SAI>
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 TCPLHQFRCDN--GHCIEMGRVCNHVDDCSDNSDEKGCGINECLDSSISRCDHNCTDTIT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFYCSCLPGYKLMSDKRSCVDIDECKESPQLCSQKCENVVGSYICKCAPGYIREPDGKSC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- LLRDCISCASI -- CGQHPKQCAYFCENKLRSPV - NLPPELRRQRSGEVE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LLRDCISCASI--CGQHPKQCAYFCENKLRSPV-NLPPELRRQRSGEVE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCPEEQY-WDPLLGTCMSCKTICNHQ---SQRTCAAFCRSLSCRKEQGKFYDH----- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                     F:884-921/Domain: LDL receptor ligand-binding repeat homology <LDLE>
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F:1236-1235/Domain: EGF homology <EGG>
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                                                  <US
                                                                                  <LDL7>
           <TDIT6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
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760-794/Domain: LDL receptor ligand-binding repeat homology 799-833/Domain: LDL receptor ligand-binding repeat homology 843-89/9/Domain: LDL receptor ligand-binding repeat homology 884-921/Domain: LDL receptor ligand-binding repeat homology 929-963/Domain: LDL receptor ligand-binding repeat homology
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63;
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Pred. No. 25;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 NNSDN-----SGRY--QGLEHRGSEASPALPGL 153
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Best Local Similarity
Matches 40; Conserv
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Best Local Similarity
       F;760-794/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
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11;

Gaps

RICAAFCRSLSCRK 73

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hypothetical protein yhjo - Bacillus subtilis
C;Species: Bacillus S; Bruschi, C;V; Caldwell, B; Capuano, V; Carter, N.M.;
A; Ehrlich, S;D; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, M.; Fujita, M.; Fubita, S; Galizzi, A.; Gal
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, K.; Lapidus, A.; Lardino
A;Authors: Canduger, D.; Razarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogdwa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schlaich, S.; Schroeter, R.; Scoffone, F.; Sekliguchi, J.; Sekwaska, A.; Sea
Akauthors: Schlaich, S.; Schroeter, R.; Scoffone, F.; Sekliguchi, J.; Sekwaska, A.; Sea
Akauthors: Schlaich, S.; Schroeter, F.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: H69834
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB;GN00023; CESP:T23F1.6
A;Experimental source: clone T23F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T23F1.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T25169 R;Wilkinson, J. Submitted to the EMBL Data Library, October 1996 A;Reference number: 219990 A;Reference number: 219990
                                                                 654 EEEEEY-----TGVCHPECGDKGCDGPSADQCLNCVHFSLGNSKTNRKCVSEC----- 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EQYSEACIEACIDCMKACNHCFTKCLEESVQHHLSGCIRLDRECADICALAVKAMQTDSP 61
                                                                                                                                       74 EQGKFYDHLLRDCISCASIC----GQHPKQC-----AYFCENKLRSPVNLPP 116
                                                                                                                                                                                   A; Residues: 1-108 <KUN>
A;Cross-references: GB:Z99109; GB:AL009126; NID:g263326Q;
A;Experimental source: strain 168
DQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCK - -TICNHQSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 -----AFCRSL--SCRKEQGKF-YDHLLRDCISCASICGQHPKQ¢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 FMKEICALCADICEACGTECGKHDHDH----CQACAKACFTCAEQC
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Pred. No. 3.5;
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A;Molecule type: DNA
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Best Local Similarity 23.6%;
Matches 25; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
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16
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                                                                                                                                                                                                                                                                                                                                         A Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C; Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin type C; Superfamily: protein-tyrosine kinase, receptor type tie; bgF homology; fibronectin type K; 12-22, Domain: signal sequence #status predicted <SIG>
F; 23-1124/Product: protein-tyrosine kinase, receptor type tek #status predicted <MAT>
F; 37-104/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;830-838/Region: protein kinase ATP-binding motif
F;140,158,399,438,464,560,596,649,691/Binding site: carbohydrate (Asn) (covalent) #statu
F;855,872,964/Active site: Lys, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Rattus norvegicus (Norway rat)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C; Accession: 153282
R; Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Mains, R.E.
Endocrinology 135, 1178-1185, 1994
A; Title: PACE4: a subtilisin-like endoprotease prevalent in the anterior pituitary and A; Reference number: 153282; MUID: 94349873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTCKERCSG-----DEGCKSYVFCLPDPYGCSCATGWKGLQCNEACH-----PGFYGPDCK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                            A; Cross-references: GB:L06139; NID:9292823; PIDN:AAA61139.1; PID:9292824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:L31894; NID:9496221; PIDN:AAA61987.1; PID:9496222
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C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F;117-415/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%; Score 81; DB 1; Length 1124; 24.2%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F.364-426/Domain: Immunoglobulin homology <IM2>
F.447-527/Domain: fibronectin type III repeat homology <FN3A>
F.542-625/Domain: fibronectin type III repeat homology <FN3B>
F.542-625/Domain: fibronectin type III repeat homology <FN3B>
F.322-720/Domain: fibronectin type III repeat homology <FN3C>
F.322-722/Domain: transmembrane #status predicted <TMM>
F.322-1099/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 RQRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQV 160
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-937 < RES.
                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;135-137/Region: cell attachment (R-G-D) motif
F;211-251/Domain: EGF homology <EG1>
F;252-298/Domain: EGF homology <EG2>
F;302-340/Domain: EGF homology <EG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 80.5; Dilarity 24.1%; Pred. No. 21; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 22;
15; Mismatches
                                                                                                                                                                                                                                      A; Cross-references: GDB:344185; OMIM:600221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 WTGVAMRSCPEEQYWDP----LLGTCM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.28
Matches 39; Conservative
                                                                                                                                                                                                                                                                           A; Map position: 9p21-9p21
                                                      A; Molecule type: mRNA
A; Residues: 1-1124 <RES>
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Best Local Similarity
Matches 27; Conserv
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PIDN:CAB12900.1; PID:e11830

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46;

26;

100

Length 108;

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A;Introns: 16/3
C;Superfamily: gliadin
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8 33 SCPEEQYWDPLLGTCM----SCKTIC----NHQSQRTCAAFCRSLSCRKEQG---KFYD 80 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 58 SCASSQQYQLQTSQCMPACQQSCSQQCQSNTNTQCQPTCQQSCQTSSCNPMTSTPIPASQ 117 Query Match 8.8%; Score 80; DB 2; Length 330; Best Local Similarity 24.6%; Pred. No. 9.4; Matches 33; Conservative 14; Mismatches 55; Indels 32; Gaps 132 NSGRYQGLEHRGSE 145 | :| | :| : 167 NQMQYGGYNQOGNQ 180 qq δ 셤 ò ò

Search completed: June 25, 2002, 16:13:25 Job time: 125 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 25, 2002, 16:22:42; Search time 27:55 Seconds (without alignments) 233:301 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-854-864-15 909 1 MSGLGRSRRGGRSRVDQEER.....SPALPGLKLSADQVALVYST 166

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues

Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	D	K5_MOUSE Q04592 mus		AN Q92824 homo	P98158	AN	Q63415 rattu	AN Q13751	P98163	014258	061554		SE Q61129		ST	92509	MOUSE	P29122 homo	HUMAN P35555 homo	Q07954 homo	MOUSE P39429 mus m		TIE2_BOVIN Q06807 bos taurus		LMA3_MOUSE Q61789 mus musculu		MOUSE	SE	P79377 sus		HUMAN P98160	CAEEL 002151	
	DB ID	1 1	1 A		1 L				1 Y	1 2	 F	<u>ب</u>	1 C	1 P	1 Y] 									_							7 Z	
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æ	Query Match	10	9.1	9.1	9.0	6.8	6.8	8.7									8.3	8.3	8.3	8.3	8.3	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.0	8.0	8.0	•
	Score	7.5	83	82.5	82	81	80.5	79.5	79.5	78.5	77.5	76.5	97	16	75.5	75	75	75	75	75	74.5	74.5	74	74	74	m	73.5	3	73	73	73	72.5	
	Result No.	1	7	e	7	'n	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	ç

P18564 homo sapien Q9nj15 branchiosto P1378 homo sapien P36184 entamoeba h O43915 homo sapien P50555 sus scrofa P20736 boophilus m P20662 mus musculu P2448 caenorhabdi P14585 caenorhabdi P97927 mus musculu		rsor (EC 3.4.21) protease PC5) convertase 6)	Euteleostomi; ; Murinae; Mus.	ge Cys-rich region	Murakami K., new member of the ily: its striking	i., Seidah N.G.; in-like PC5: a ine and	Nakayama K., ed to different	are coexpressed with bone
34 72.5 8.0 788 1 ITB6_HUMAN 35 72.5 8.0 1696 1 PCK5_BRACL 37 7.9 290 1 HXD8_HUMAN 38 72 7.9 308 1 ACP1_ENTHI 39 72 7.9 461 1 TRIA_EPIG 40 72 7.9 461 1 TRIA_EPIG 41 72 7.9 783 1 ZFY2_MOUSE 42 72 7.9 1068 1 AFIO_MOUSE 43 72 7.9 1068 1 AFIO_MOUSE 44 72 7.9 1429 1 LIT2_CAEEL 45 72 7.9 1816 1 LMAA_MOUSE	ALIGNMENTS RESULT 1	PCK5_MOUSE ID PCK5_MOUSE AC 004592; Q62040; DT 01-FEB-1995 (Rel. 31, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last sequence update) DF 16-OCT-2001 (Rel. 40, Last sequence update) DF 16-OCT-2001 (Rel. 40, Last sequence update) DF PCOPTOTEIN CONVERTISES SUBTILISIN/Kexin type 5 precu DE (Proprotein convertase PC5) (Subtilisin/Kexin-like DE (SPC6) CONVERTISE PC5) (PC6) (Subtilisin-like proprotein CN PCSN5)	OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; OC Mammalla; Butheria; Rodentia; Sciurognathi; Muridae OX NCBI_TaxID=10090;		SEGUENCE FROM N.A. (ISOFORM PC5A). TISSUE-Brain, and Intestine; TISSUE-Brain, and Intestine; TISSUE-3324489; Pubmed-8468318; Nakayama K.; Nakayama K.; "Identification and functional expression of a mammalian Kex2-like processing endoprotease fam structural similarity to PACE4"; J. Biochem. 113:132-135(1993).		RN 14) RN 14) RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION. RX MEDLINE-97103178; PubMed-8947550; RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., RA Bendayan M., Seidah N.G.; RT "The isoforms of proprotein convertase PC5 are sor RT subcellular compartments."; RL J. Cell Biol. 135:1261-1275(1996). RP DEVELOPMENTAL EXPRESSION.	MEDLINE=96293359; PubMed=8698813; Constam D.B., Calfon M., Robertson E.J.; "SPC4, SPC6, and the novel protease SPC7

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                                                                                                                                                                                                                                                                                                                                                                                            -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE)
AND PC5A/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: PC5A IS EXPRESSED IN MOST TISSUES BUT IS MOST
ABUNDANT IN THE INTESTINE AND ADRENALS. PC5B IS EXPRESSED IN THE
INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
-1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBKYO.
EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
E5.5, INTENSE EXPRESSION IN EXTRABBRYONIC ENDODERM, AND
NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
SAC FOLLOWED BY A CONFINATION TO DERMANOTOME COMPARTMENT. BETWEEN
E9.5 AND E11.5, ABUNDANT EXPRESSION IN THE LINBS IS CONFINED
TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL.
CRELLS OF LIMB BUDS), AT E12.5, EXPRESSION IN THE LINBS IS CONFINED
TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL.
CARTILAGE PRINORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
CARTILAGE PRINORDIA AND IN THE MUSCLE OF THE INTESTINAL VILLI.
ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
ISOFORM B OCCUR AT E12.5
ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  MEDLINE=97436919; PubMed=9291583;
Rancourt S.L., Rancourt D.E.;
Rancourt S.L., Rancourt D.E.;
"Mutine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";
Dev. Genet. 21:75-81(1997).
-!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROLINESTINAL PEPTIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
                                                                                                                                                                                                                                                                                                           CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
SUBCELLUIAL ROCATION: PCSA IS SECRETED THROUGH THE REGULATED
SECRETORY PATHRAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS WITH THE TGN SORTING PROTEIN PACS-1.
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morphogenetic proteins at distinct sites during embryogenesis.", J. Cell Biol, 134:181-191(1996),
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InterPro; IPR002174; Furin-like.
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                                                      DEVELOPMENTAL EXPRESSION.
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MEROPS; S08.076; -
MGD; MGI:97515; PC
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                                                                                                                                                                                                                                                                                                                                                                                  PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
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                                          Probom; prof. Prof
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01-DEC-1992 (Rel. 24, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Apomucin (Mucin core protein) (Fragment).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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1877 AA; 209287 MW; EC850E2DF20EALC3 CRC64;
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Pfam; PF00082; Peptidase_S8; 1.
                         PRINTS; PR00723; SUBTILISIN. ProDom; PD000717; P.domain;
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IPR002884; P_domain. IPR000209; Peptidase_S8

InterPro; InterPro; InterPro;

Pfam; PF01483; P; 1.

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PROSITE; PS01208; VWFC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES OF RESIDUES WHICH HAVE GLY AT POSITION APPEARS TO OCCUR ON SER RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE GLYCOSYLATION SITE OR, WHENE GLY IS THE PENULTHMATE RESIDUE. THE PRESENCE OF PROLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENHANDE GIYCOSYLATION.
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Submaxillary gland,
MEDLINE-97248516; PubMed-9102502;
MEDLINE-97248516; PubMed-9102502;
MEDLINE-97248516; PubMed-9102502;
MEDLINE-97248516; PubMed-9102502;
Gerken T.A., Owens C.L., Pasumarthy M.;
Determination of the site-specific O-qiycosylation pattern of the portion submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:gaplane transferase peptide binding site.";
J. FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY WICCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUECUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBGUNT: INTERMOLECULAR DISULFIDE BONDS COULD HELP MAINTAIN A MULTIMERIC MUCIN STRUCTURE.
SUBGELLULAR LOCATION: SECRETE SECRETE INTERSECTION SPECIFICATY: SUBMAXILLARY MUCOSAE.
DOMAIN: CONTAINS TANDEMLY REPEATED, IDENTICAL SEQUENCES OF 81
                                                                                                                                                                                                                                                                                                    TISSUE-Submaxillary gland;
MEDLINE-87280230; PubMed-3611111;
Eckhardt A.E., Timpte C.S., Abernethy J.L., Toumadje A.,
Johnson M.C. Jr., Hill R.L.;
"Structural properties of porcine submaxillary gland apomucin.";
J. Biol. Chem. 262:11339-11344(1987).
                                                                                                                                                                                                        Timpte C.S., Eckhardt A.E., Abernethy J.L., Hill R.L.;
"Porcine submaxillary gland apomucin contains tandemly repeated, identical sequences of 81 residues.";
J. Biol. Chem. 263:1081-1088(1988).
                                         TISSUE-Submaxillary gland;
MEDLINE-91236743; PubMed-2033060;
BCkhardt A.B., Timpte C.S., Abernethy J.L., Zhao Y., Hill R.L.;
"Porcine submaxillary much contains a cystine-rich, carboxyl-terminal domain in addition to a highly repetitive,
                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYDRATE-LINKAGE SITES, AND SEQUENCE OF 45-125
                                                                                                                      glycosylated domain.";
J. Biol. Chem. 266:9678-9686(1991)
                                                                                                                                                               SEQUENCE OF 1-503 FROM N.A.
TISSUE-Submaxillary gland;
MEDLINE-88087170; PubMed-2826455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A40009; A40009.
InterPro; IPR000359; Cys. knot.
InterPro; IPR001007; VWFC.
Pfam; PF00007; Cys.knot; 1.
SMART; SM00041; CT; 1.
PMOSITE; PS01185; CTCK.1;
PROSITE; PS01185; CTCK.2; 1.
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                              SEQUENCE FROM N.A
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(MUCIN TYPE).
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                              81 AA TANDEM REPEATS.
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C-LINKED (GALNAC.

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VWFC.
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Best Local Similarity 23.5%; Pred. No. 2.7;
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     PCK5_HUMAN
PCK5_HUMAN

PCK5_HUMAN

AC Q92824; Q13527;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DF 16-OCT-2001 (Rel. 40, Last annotation update)

DF 16-OCT-2001 (Rel. 40, Last annotation update)

DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)

DE (Convertase PC5) (PC6) (hPC6).
                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: EXPRESSED IN T-LYMPHOCYTES.
DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
                                                                                                                                                                                                                         Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; "Isolation of the human PC6 gene encoding the putative host protease for HIV-1 gp160 processing in CD4+ T lymphocytes."; Proc. Natl. Acad. Sci. US.A. 93:7695-7700(1996).
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                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                            Lu Y., Duke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                                                                                         Frankland A., Miranda L., Wolf J., Pichuantes S., Lu Y. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002884; P_domain.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR00082; Peptidase_S8.
InterPro; IPR0073; SUBTILISIN.
IPRODOM; IPR00073; SUBTILISIN.
IPRODOM; IPR00073; P_domain; I.
SMART; SM00261; FU; 5.
                                                                                                                                                                                                              MEDLINE=96353880; PubMed=8755538;
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 15-913 FROM N.A.
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                                                                                                                      PCSK5 OR PC5 OR PC6.
Homo sapiens (Human)
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01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E., Norris K., Gliemann J., Christensen E.I.; "Evidence that epithelial glycoprotein 330/\text{megalin} mediates uptake of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                    CYS. RICH MOTIF (CRM) REGION.
CLEAVAGE (AUTO-) (BY SIMILARITY).
CLEATACHMENT SITE (POTEWITAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTEWITAL).
                                                                           PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
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Y -> A (IN REF. 3).

R -> A (IN REF. 3).

R -> C (IN REF. 3).

21389264CAD7546C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.1%; Score 82.5; DB
26.0%; Pred. No. 2.4;
ive 10; Mismatches
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on pair of basic residues; Repeat.
                            BY SIMILARITY
BY SIMILARITY
                                                                                                                               CATALYTIC.
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MEDLINE-95024033; PubMed-7937880;
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J. Clin. Invest. 96:1404-1413(1995)
                                                                                                        TYPE
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913 AA;
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Matches 27; Conserv
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EGF-LIKE 3.

LDL-RECEPTOR CLASS B 61

LDL-RECEPTOR CLASS B 81

LDL-RECEPTOR CLASS B 81

LDL-RECEPTOR CLASS A 91

LDL-RECEPTOR CLASS A 11

LDL-RECEPTOR CLASS B 12

LDL-RECEPTOR CLASS B 13

LDL-RECEPTOR CLASS B 14

EGF-LIKE 9.

LDL-RECEPTOR CLASS B 14

EGF-LIKE 9.

LDL-RECEPTOR CLASS B 14

LDL-RECEPTOR CLASS B 24

LDL-RECEPTOR CLASS B 34

LDL-RECEPTOR CLASS B 34

LDL-RECEPTOR CLASS B 34

LDL-RECEPTOR CLASS B 34

LDL-RECEPTOR CLASS A 31

LDL-REC
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LDL-RECEPTOR CLASS B
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
A cheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D., Andres G., McCluskey R.T.;

Andres G., McCluskey R.T.;

Torgan distribution in rats of two members of the low-density
"Ipoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
receptor-associated protein (RAP).";

J. Histochem. Cytochem. 42:531-542(1994).

J. Histochem. Cytochem. 42:531-542(1994).

J. Histochem. Cytochem. 42:531-542(1994).

COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
LACTOFERRIN, CLUSTERIN AND CALTVATOR INHIBITOR TYPE I
COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
COMPLEX, APOLIPOROTEIN B-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
COMPLEX, APOLITIN AND CALCIUM.

COMPLEX ADOLITINER OF COMPLEX TOGETHER WITH A RECEPTOR-
COMPLEX ASSOCIATED PROTEIN (RAP).

COMPLEX SACCIATED PROTEIN (RAP).

CLATRIN-COAPTAINS A SOLUBLE FORM IS POSSIBLY DERIVED BY
CLATRIN-COAPTAINS A SOLUBLE FORM IS POSSIBLY DERIVED BY
CLATINAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.

COLORIANAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.

CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.

CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
                                                                                                                                                                                                                                                                                                                                 PROTEIN 2.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 7.
BGF-LIKE 1.
BGF-LIKE 1.
BGF-LIKE 2.
LDL-RECEPTOR CLASS B 1.
LDL-RECEPTOR CLASS B 1.
LDL-RECEPTOR CLASS B 1.
LDL-RECEPTOR CLASS B 2.
LDL-RECEPTOR CLASS B 3.
LDL-RECEPTOR CLASS B 4.
                                                                                                                                                                                                                                                                                                                       EMBL; L34049; AAA51369.1; -. HSSP; Q07954; 1CR8.
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44426
44426
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1145
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DOMAIN
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MEDLINE=91134665; PubMed=8980225;
Wikkulla M.; Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J.,
Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
Mulliken J.B., Olse B.R.;
"Vascular dysmorphogenesis caused by an activating mutation in the
receptor tyrosine kinase TIE2.";
[3]
                                                                                                                                                                                                                                            3134 SFYCSCLPGYKLMSDKRSCVDIDECKESPQLCSQKCENVVGSYICKCAPGYIREPDGKSC 3193
                                                                                                                                                                                                                                                                   ------LLRDCISCASI -- CGQHPKQCAYFCENKLRSPV-NLPPELRRQRSGEVE 127
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                 33 SCPEEQY-WDPLLGTCMSCKTICNHQ---SQRTCAAFCRSLSCRKEQGKFYDH----- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R., "Molecular cloning and characterization of a novel receptor protein
                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Anglopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein Kinase receptor TIE-2) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TIE) (Tyrosine-protein kinase receptor TEK) (P140
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
              EGF-LIKE 16.
EGF-LIKE 17.
EGF-LIKE 17.
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                  36,
                                                                                   ENDOCYTOSIS SIGNAL (POTENTIAL). ENDOCYTOSIS SIGNAL (POTENTIAL).
                                                                                                                                                                                                 DB 1; Length 4660;
                                                                                                                                                                                                                  64; Indels
а а
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                                                                                                                                                                                                                                                                                                     128 NNSDN-----SGRY--QGLEHRGSEASPALPGL 153
                                                                                                                             SIMILARITY. SIMILARITY.
                                                                                                                       SIMILARITY.
                                                                                                                                                                       SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                 15; Mismatches
                                                                                                                                               SIMILARITY
LDL-RECEPTOR
LDL-RECEPTOR
                                                                                                             SIMILARITY
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                                                                                                                                                                                                         Pred. No. 13;
                                                                                                                                                                                                 Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine kinase from human placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93173509; PubMed-8382358;
                                                                                                     BY
BY
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                                                                                                                                                                                                                  Conservative
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4460
4463
4625
4625
1745
4527
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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TISSUE-Placenta;
                                                                                                                                                                                                          Local Similarity
                                44454
445454
44506
44509
44509
44502
350
447
744
1108
1408
1409
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                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYTOSINE phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
AND THEIR PROCENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
BALFORMATIONS (WOMI), AN ERROR OF VASCULAR WORPHOGENESIS
CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN.
VARIANTS VMCMI TRP-849 AND SER-897.

MEDLINE=99299243; PubMed=10369874;

Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prietto V.G.,
Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A.,
Speer M.C., Peters K.G., Marchuk D.A.;

"Allelic and locus heterogeneity in inherited venous malformations.";
Hum. Mol. Genet, 8:1279-1289(1999).

- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER PROBABLY REGULATES
ENDOTHELIAL CELL PROLIFERRATION, DIFFERRATION AND GUIDES THE
PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00102; EGF_1; 3.
PROSITE; PS00186; EGF_2; 3.
Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family; Disease mutation.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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EGF-LIKE 2.
EGF-LIKE 3.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; FN_III.
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Pfam; PF000069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
SMART; SM00181; EGF; 2.
SMART; SM00001; EGF_11ke; 1.
SMART; SM00000; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L06139; AAA61139.1; -.
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MIM; 600195;
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MEDLINE=94349873; PubMed=8070361;
Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
"PACE4: a subtilisin-like endoprotease prevalent in the anterior pituitary and regulated by thyroid status.";
Endocrinology 135:1178-1185(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: LIKELY TO REPRESENT AN ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE SECRETORY PARHWAY, WITH UNIOUS RESTRICTED DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES AND CAPPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-!-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
-:- COFACTOR: PROBABLY CALCIUM-DEPENDENT (BY SIMILARITY).
-:- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE ANTERIOR PITUITARY AND IN SEVERAL BRAIN REGIONS, THE ATRIUM, AND THE VENTRICLE.
-:- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPPERONE
                                                                                                                                                                                                                                                                                     RTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELR 119
                                                                                                                                                                                                                                                                                                                                     262 RTCKERCSG----QEGCKSYVFCLPDPYGCSCATGWKGLQCNEACH-----PGFYGPDCK 312
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                           ----SCKTICN-HOSO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Paired basic amino acid cleaving anzyme 4 precursor (EC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                            -> S (IN VMCM1; ACTIVATING EFFECT).
                                                                                                                                                   R -> W (IN VWCM1; ACTIVATING EFFECT).

//FIId=VAR_006352.

Y -> S (IN VMCM1 ACTIVATING FFFECT).
                                                                        (POTENTIAL).
                                                                                  (POTENTIAL).
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                                                                                                                                    (POTENTIAL).
                                                             (POTENTIAL)
                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                 DB 1; Length 1124;
                                                                                                                                                                                                                                                      63; Indels
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                                                                              (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
 FIBRONECTIN TYPE-III 3.
                                                                       (GLCNAC. . .)
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                   SIMILARITY).
                              (BY SIMILARITY).
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Pred. No. 4.1;
5; Mismatches
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through a collaboration the EMBL outstation - to restrictions on its content is in no way by and for commercial
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   654 EEEEEY----TGVCHPECGDKGCDGPSADQCLNCVHFSLGNSKTNRKCVSEC----- 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCK--TICNHQSQRTCAAFCRSLSCRK 73
                                       SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL ATTACHMENT SITE POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
  ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 EQGKFYDHLLRDCISCASIC----GQHPKQC-----AYFCENKLR$PVNLPP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLGYFGDTAARRCRCHKGCETCTGRSPTQCLSCRRGFYHQETNTCVTLCP 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F3865557C33705C8 CkC64;
ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMB3_HUMAN STANDARD; PRT; 1172 AA. 013751; 014733; 014947; 09UJK4; 09UJL1; 014V-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NAR-2002 (Rel. 41, Last annotation update) Laminin beta-3 chain precursor (Laminin 5 beta 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO B.
CYS-RICH MOTIF (CRM)
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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24.1%; Pred. No. 3.8;
ive 17; Mismatches
                                                                                  SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000209; Peptidase_S8
Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002174; Furin-like.
InterPro; IPR002884; P_domain.
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937 AA;
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COMPONENT).

OMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COLLED COLL STRUCTURE.

DOMAIN: DOMAIN VI IS GLOBULAR.

DOMAIN: DOMAIN VI IS GLOBULAR.

BUSEARSE: DEFECTS IN LAMBS ARE A CAUSE OF JUNCTIONAL EPIDERMOIYSIS

BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A

BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
                                                                                                                                                                                                                                                                                             MEDLINE-21221101; PubMed-11296269; Robbins P.B., Lin Q., Goodnough J.B., Tian H., Chen X., Khavari P.A.; "In vivo restoration of laminin 5 beta 3 expression and function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96055522; PubMed-7550237; Pulkkinen L., McGrath J.A., Christiano A.M., Uitto J.; Puckrethon C., McGrath J.A., Christiano A.M., Uitto J.; Detection of Sequence variants in the gene encoding the beta 3 chain of I laminin 5 (IAMB3)."; Hum. Mutat. 6:77-84(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                              Ή.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Epidermis;
MEDLINE-96015057; PubMed-8530036;
Morishima Y., Ariyama T., Yamanishi K., Abe T., Ueda E., Yasuno
                                                                                                                                ø
                                                                                                                                                                                                             Gerecke D.R., Wagman D.W., Champliaud M.F., Burgeson R.E.; "The complete primary structure for a novel laminin chain, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELÍULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                                                                                                               Burgeson R.E., Uitto J., "Composite of the beta 3 chain gene (LAMB3) of human laminin 5, candidate gene in junctional epidermolysis bullosa."; Genomics 25:192-198(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Chromosomal loci of 50 human keratinocyte cDNAs assigned by fluorescence in situ hybridization."; Genomics 28:273-279(1995).
                                                        [1]
SEQUENCE FROM N.A.
MEDLINE-95293372; PubMed=7774918;
Pulkkinen L., Wagman D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                          junctional epidermolysis bullosa.";
Proc. Natl. Acad. Sci. U.S.A. 98:5193-5198(2001).
                                                                                                                                                                     [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 172-190.
MEDLINE-94209274; PubMed-7512558;
                                                                                                                                                                                                                                                       J. Biol. Chem. 269:11073-11080(1994).
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VARIANT GABEB LYS-210
sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [6]
VARIANT JEB LEU-679.
                                                                                                                                                                                                                                          laminin Bik chain."
                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grafham D.;
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                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
SIMILARITY: CONTAINS 6 LAMININ EGF-LIKE DOMAINS.
                     NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERWOLYSIS BULLOSA.
                                                                                                          BENIGN EPIDERMOLYSIS BULLOSA (GABEB). THIS NONLETHAL FORM OF JUNCTIONAL EPIDERMOLYSIS BULLOSA IS CHARACTERIZED BY LIFE-LONG BLISTERING OF THE SKIN, ASSOCIATED WITH HAIR AND TOOTH
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                                                                                         DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF GENERALIZED ATROPHIC
BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMININ BETA-3 CHAIN.
LAMININ NTERMINAL (DOMAIN VI).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Basement membrane; Extracellular matrix; (Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Disease mutation; Epidermolysis bullosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN ALPHA.
DOMAIN I.
COILED COIL (POTENTIAL).
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PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC51352.1; JOINED.
AAC51352.1; JOINED.
AAC51352.1; JOINED.
AAC51352.1; JOINED.
AAC51352.1; JOINED.
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Pfam; PP00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
ProDom; PD002082; Lamin; 1.
SNART; SM00180; EGF_Lam; 6.
SWART; SM00180; Lamin; 1.
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InterPro; IPR001886; LamNT.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC51352.1; JOINED AAC51352.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D37766; BAA22263.1; -. AL031316; CAB40149.1; -. AL023754; CAA19297.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L25541; AAA61834.1; -. AY035783; AAK61364.1;
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AAC51352.1;
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AAC51352.1;
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                                                                                                                                                                                  ABNORMALITIES.
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U17754;
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PROSITE;
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CITCHASMIC (POTENTIAL).

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 5.

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 4.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 6.

LDL-RECEPTOR CLASS A 7.

LDL-RECEPTOR CLASS A 7.

LDL-RECEPTOR CLASS A 9.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS A 12.

LDL-RECEPTOR CLASS A 12.

LDL-RECEPTOR CLASS A 13.

EGF-LIKE 5.

EGF-LIKE 5.

EGF-LIKE 5.
       Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                      superfamily.";
                                                                                                                                                             Schonbaum C.P., Lee S., Mahowald A.P.;

"The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the low density lipoprotein receptor guperfamily.";

Proc. natl. Acad. Sci. U.S.A. 92:1485-1489(1995).

-! FUNCTION: INVOLVED IN UPTAKE OF VITELLOGENIN BY ENDOCYTOSIS.

-! STATICARITY: COWNAINS 13 LDL-RECEPTOR CLASS A DMAINS.

-! SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Transmembrane; EGF-like domain; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUTATIVE VITELLOGENIN RECEPTOR.
EXTRACELLULAR (POTENTEAL).
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InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR000172; EDL_recept_A.
InterPro; IPR00003; EGF_Ca.
Pfam: PF00008; EGF; 5.
Pfam: PF00008; Idl_recept_b; 6.
PRIMTS; PR00179; EGF_CA; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00192; LDLafte; 4.
SMART; SM00192; LDLafte; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; iPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                TISSUE=Ovary;
MEDLINE=95183490; PubMed=7878005;
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PROSITE; PS01187; EGF_CA, 2.
PROSITE; PS01209; LDLRA_1; 11.
PROSITE; PS50068; LDLRA_2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U13637; AAB60217.1; -. HSSP; P07204; 1ADX.
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N-LINKED (GLCNAC...) (POTENTIAL).
N-N (IN GRE. 2).
MISSING (IN REF. 2).
N-N (IN REF. 2).
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55.3%; Pred. No. 5.9;
ve 16; Mismatches 66; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> P (IN REF. 2).
G -> A (IN REF. 2).
MW; 61BC1A60BD4FA05 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
VL OR YOLKLESS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indue S., Orimo A., Hosol T., Kondo S., Toyoshima H., Kondo T., Ikegami A., Ouchi Y., Orimo H., Muramatsu M.; Ikegami A., Ouchi Y., Orimo H., Muramatsu M.; Genomic binding-site cloning reveals an estrogen-responsive gene that encodes a RING finger protein."; Proc. Natl. Acad. Sci. U.S.A. 90:11117-11121(1993).

-: FUNCTION: MEDIATES ESTROGEN ACTION. IN VARIOUS TARGET ORGANS.
-: SIMILARITY: CONTAINS I RING-TYPE ZINC FINGER.
                                                                                                                                                             Gaps
                                                                                                                                               WTGVAMRSCPEEQYWDPLLGTCMSCKTICN------70SQRTCAAFCRSLS-----70
                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
2inc finger protein 147 (Estrogen responsive finger protein) (Efp).
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                       27;
                                                                                                  Length 1984;
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                                                    V -> I.
MW; F92A256E0ACD5E48 CRC64;
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                                                                                               Score 79.5; DB Pred. No. 9.9; 7; Mismatches
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INTM, 600453. -

INTERPLO; IPR001870; Gamma_carbxylse.

INTERPLO; IPR001870; SPRY.

INTERPLO; IPR001871; SPRY.

INTERPLO; IPR001841; Znf_ring.

R Pfam; PF000622; SPRY; 1.

R Pfam; PF00007; Zf_C3HC4; 1.

SMART; SM00184; RING; 1.

DR PROSITE; PS0018; ZF_RING_1; 1.

AN Zinc-finger; Coiled coil. Z; 1.
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STRAILM-CD-1; TISSUE-Kidney;
Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
Submitted (ARR-1995) to the ENBL/GenBank/DDBJ databases.
Submitted (ARR-1995) to the ENBL/GenBank/DDBJ databases.
-! FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILLIN-1-CONNECTIVE TISSUE MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
-! PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER FIBRILLIN INDLECULES OR WITH OTHER COMPONENTS OF THE MICROFIBRILS (BY SIMILARITY).
-! SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING
                                                                                                                                                                                 73 KEQGKFYDHLL----RDCISCASICGQHPKQCAYFC------ENKLRSPVNLP 115
                                                                                                                                                                                                                     FDSPAFQDHPLOPPVRDLL--RRKCSQHNRLREFFCPEHSECICHICLVEHKTCSPASL- 191
                                                                                                                                            86 PADVWTPPARASAPSP-----NAQVACDHCLKEAAVKTCLVCMASFCQEHLQPH 134
                                                                                                         22 PQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNH----QSQRTC----AAFCRS-LSCR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95130561; PubMed=7829516;
MEDLINE-95130561; PubMed=7829516;
Xin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,
Pereira L., Ramirez F., Bonadio J.;
Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene.;
J. Biol. Chem. 270:1798-1806(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                    53;
                                   Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                      54; Indels
                                                                                                                                                                                                                                                          116 PELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQV 160
                                                                                                                                                                                                                                                                                   ----SQASADLEAT------LEHKLIVMYSQINGASRALDDV 223
                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                               FBN1_MOUSE STANDARD; PRT; 2871 AA. 061554; Q60826; Clandard; Cland
                               Query Match 8.6%; Score 78.5; D
Best Local Similarity 23.0%; Pred. No. 4;
Matches 38; Conservative 20; Mismatches
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InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002121; TB.
Pfan; PF00008; EGF; 46.
Pfam; PF00683; TB; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L29454; AAA56840.1; -. EMBL; U22493; AAA64217.1; -. HSSP; P35555; LAPJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:95489; Fbn1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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FBN1_MOUSE
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DISULFID	2011	DISGUETD

REDINE-92381035: PubMed-1512259;
Rebine-92381035: PubMed-1512259;
Rebine-92381035: PubMed-1512259;
Rebine-92381036: PubMed-1512259;
Repeated M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
Rentrop M., Gateff E.A.F., Leunissen J.B.M., van de Ven W.J.;
Repeats of a cysteine motif.";
Repeats of mature proteins from their can be any amino acid and Yea is Arg or Lys. Releases albumin,
Complement component C3 and von Willebrand factor from their This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 9 Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila. Gaps 1 MSGLGRSRR------GGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMS 49 50 CKTICNH-------QSQRTCAAFCRSLSCRKEQGKFYDHLLRDCI--------87 respective precursors. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY. FURIN SUBFAMILY. 63; Score 77.5; DB 1; Length 2871; Pred. No. 22; 33; Indels 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2). PRT; 1680 AA. 14; Mismatches BY SIMILARITY BY SIMILARITY Fiybase; FBGN0004598; Fur2. InterPro; IPR000561; BGF-11ke. InterPro; IPR00174; Furin-11ke. InterPro; IPR002884; P_domain. InterPro; IPR001209; Peptidase_S8. Pfam; PF00757; Furin-11ke; 1. 2440 TSCVDLNECNQAPKPCNFICKN 2461 88 -SCASI--CGQHPKQCAYFCEN 106 PF00082; Peptidase_S8; 1. Query Match
Best Local Similarity 22.5%; EMBL; M94375; AAA28551.1; -. 32; Conservative STANDARD; PIR; A43434; A43434. HSSP; Q99405; 1MPT. SEQUENCE FROM N.A. 1652 1658 FUR2_DROME P30432; DISULFID DISULFID Pfam; Pfam; FUR2_DROME Matches qq δ g FT δλ

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homologue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 -EQGKFYDHLLRDCISCASICGQHPKQCAYFCENKL-RSPVNLPPELRRQRSGEVENNSD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFAI_MOUSE STANDARD; PRT; 603 AA.
601129; 0508007;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Complement factor I precursor (EC 3.4.21.45) (C3B/C4B inactivator).
IF OR CFI.
                                                                                                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
, CYS-RICH.
                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. )) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTGVAMRSCPEEQYWDPLLGTCMSCKTICNH-QSQRTCAAFCRSLSCRK------
                                                                                                                                                                                                                                                                                    (POTENTIAL).
Prints; PR00723; SUBTILISIN.
Prodom; Pr000717; P_domain; 1.
SMART; SM00181; EGF; 1.
SMART; SM00261; FU; 10.
PROSTIE; PS00136; SUBTILASE_ASP; 1.
PROSTIE; PS00137; SUBTILASE_ASP; 1.
PROSTIE; PS00139; SUBTILASE_BIS; 1.
PROSTIE; PS00139; SUBTILASE_SIS; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane; Multigene family; Zymogen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1680;
                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Indels
                                                                                                                                                 10 X TANDEM REPEATS,
                                                                                                 POTENTIAL.
FURIN-LIKE PROTEASE
                                                                                                                    CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.5; I
Pred. No. 16;
                                                                                          POTENTIAL.
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Best Local S:
Matches 33
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CFAI_MOUSE
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                               STRAIN=BALB/C;
MEDLINES-9617503;
PubMed=8604219;
Minta J.O., Wong M.J., Kozak C.A., Kunnath-Muglia L.M., Goldberger G.;
"CDNA cloning, sequencing and chromosomal assignment of the gene for mouse complement factor I (C3b/C4b inactivator): identification of a species specific divergent segment in factor I.";
Mol. Immunol. 33:101-112(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Mol. Biol. Int. 47:493-500(1999).
-!- FUNCTION: RESPONSIBLE FOR CLEAVING THE ALPHA-CHAINS OF C4B AND C3B
IN THE PRESENCE OF THE COFACTORS C4-BINDING PROTEIN AND FACTOR H
RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SV; TISSUE-Kidney;
MEDLINE=99220287; PubWed=10204086;
Yun Y.-S., Goldberger G., Minta J.O.;
"Cloning and characterization of the non-catalytic heavy chain of mouse complement factor I gene: structure comparis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYBEIN FAMILY.
-i- SIMILARITY: CONTAINS 1 KAZAL-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 2 LDL-RECEPPOR CLASS A DOMAINS.
-i- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: HETERODIMER OF A LIGHT AND HEAVY CHAINS LINKED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Extracellular.
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SMARY; SM00192; LDLa; 2.
SMARY; SM00192; LDLa; 2.
SMARY; SM00202; SR; 1.
SMARY; SM00202; Tryp_SPC; 1.
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
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EMBL; AF100556; AAD32955.1; -.
EMBL; AF100559; AAD32955.1; JOINED.
EMBL; AF100560; AAD32955.1; JOINED.
EMBL; AF100561; AAD32965.1; JOINED.
EMBL; AF100562; AAD32955.1; JOINED.
EMBL; AF100563; AAD32955.1; JOINED.
EMBL; AF100564; AAD32955.1; JOINED.
HSSP; P00750; 1RTF.
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InterPro: IPR001102; SRCR.
InterPro: IPR001254; Trypsin.
InterPro: IPR002350; kazal.
InferPro: IPR002350; kazal.
Infam: PP00050; kazal.
Infam: PP00057; Idl_recept_a: Infam: PP00630; SRCR: Infam: PP00089; Irypsin: Infam: PP00089; Irypsin: Infam: IPR0089; Irypsin: Infam: IPR0089; Irypsin: Infam: IPR0089; Irypsin: Infam: IPR0722; CHYMOTRPSIN.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.199; -- MEROPS; S01.199; -- MED; MGI-105937; Cfi. InterPro; IPR001314; Chymotrypsin. InterPro; IPR003884; FacI_MAC.
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PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 114-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50287; SRCR_
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SEQUENCE FROM N.A.
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       Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                     QEERFPQGL-WTGVAMRSCPEEQYWDPLLGTCMSCKTI--CNHQSQRTC-----AAFC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus.
                                                                                                                                                                                                                                     -> MGSTFLRRKPATVSMTV
                                                                            SERINE PROTESS A 2.

SERINE PROTESS A 2.

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                (POTENTIAL).

Y SIMILARITY).

Y SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PÉDIO E FROM N.A. (SHORT ISOFORM), AND TISSUE-SPECIFICITY TISSUE-Adrenal gland; MEDLINE-93342056; PubMed-8341687;
                                                                                                                                                                                                                                                                        8.4%; Score 76; DB 1; Length 603
                                                                                                                                                                                                                                                                                       Indels
                          COMPLEMENT FACTOR I.
COMPLEMENT FACTOR I HEAVY
COMPLEMENT FACTOR I LIGHT
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E2C1D43261C719E8 CRC64;
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RELAY SYSTEM (BY
RELAY SYSTEM (BY
                                                                LDL-RECEPTOR CLASS A
LDL-RECEPTOR CLASS A
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                                                                                                                                                                                                                                                                                Pred. No. 6.5;
24; Mismatches
                                                   KAZAL-LIKE
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                                                                                                                                                                                                                       CHARGE
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 TRYPSIN_SER; 1
                                                                                                                                                                                                                                                   67234 MW;
      pathway; Plasma;
                                                                                                                                                                                                                                                                               23.6%;
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                       401
                                                                                                                                                                                                                                                   603 AA;
                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 35: Concer
PROSITE; PS00135;
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                             514
555
401
449
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1114
              Repeat; Signal
       Complement
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DISULFID
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                      SIGNAL
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FOR THE MATUGATION OF GASINGIANS PETILIBES, MAY THE ACTIVATION OF GASINGIANS PROTICES, MAY THE ACTIVATION OF GASINGIANS AND ALGORITH ACTIVATION OF GASINGIANS AND ACTIVATION OF GASINGIANS AND ACTIVATION OF GASON OF AND ACTIVATION OF GASON OF ALGORITH ACTIVATION OF GASON OF ACCORDINGIAN OF ACTIVATION OF GASON OF ACCORDINGIAN OF ACTIVATION OF A SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRAND PROTEIN LOCALIZED TO A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES (BY SIMILARITY).

1-1-ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE) AND PC5A/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.

1-1-TISSUE SPECIFICITY: EXPRESSED IN THE INTESTINE, BRAIN, ADRENAL GLAND, ANTERLOR PITUITARY, THYROID, OVARIES, TESTIS AND LUNG. HIGHEST LEVELS ARE FOUND IN THE GUT, DUODENUM, JEJUNUM AND ILEUM. EXPRESSION IS HIGHER IN FEMALE THAN IN MALE REPRODUCTIVE ORGANS.

1-1-DEVELOPMENTAL STAGE: FIRST DEFECTED AT E9 IN HIGHLY RESTRICTED EXPRESSION IS HIGHER IN THE OPTIC AND OTIC VESICLES, THE ROOF OF MIDBRAIN, AND TRUNK MYOTOMES. BY MIDGESTATION (E13-E16), EXPRESSION IN THE DEPTIC AND OTIC VESICLES, THE ROOF OF MILIPIPE REGIONS IN THE DEPTICAMUS, THALAMUS, HYPOTHALAMUS, STENCE IN IN EXPERIENCE OF MILIPIPE REGIONS INCLUDING HIPPOCAMPUS, THALAMUS, HYPOTHALAMUS, STENCE DE IN THE DEPTICAMUS, PREMER STENCE IN THE DEPTICAMUS, THALAMUS, HAPPONDAIA AND THE NEW PRIMERAL ORGAN SYSTEMS, INCLUDING GUT, LUNG, ADRENAL AND EXPRINCE ORGANS. INCLUDING GUT, LUNG, ADRENAL AND EXPRINCED IN THE DEPTICAMUS, THALAMUS, ADRIBATION AND THANDAIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-97166043; PubMed-9013936;
Zheng M., Seidah N.G., Pintar J.E.;
"The developmental expression in the rat CNS and peripheral tissues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20214819; PubMed-10749928; Xiang Y., Molloy S.S., Thomas L., Thomas G.; The PC6B cytoplasmic domain contains two acidic clusters that direct socting to distinct trans-Golgi network/endosomal compartments."; Mol. Biol. Cell 11:1257-1273(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYDNEY PRIMORDIA.

DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
ASSISTING THE FOLDING OF THE 2YMOGEN WITHIN THE ENDOPLASMIC
RETICULUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACT WITH THE TGN SORTING PROTEIN PACS-1.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY 88; ALSO KNOWN AS THE
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.; Chretien M., Seidah N.G.; Chretien Conf the mouse and rat subtilisin/kexin-like PC5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells.";
                                                                                                                                                                                                                                                                                                                                                                                           Seidah N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteases PCS and PACE4 mRNAs: comparison with other proprotein
                                                                                                                                                                                                                                                                                                                                                                                      De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Sei
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                                                                                                                                                                              SEQUENCE OF 1676-1877 FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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                                                                                                                                                                                                                                                                                                                                               rissue-Adrenal gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBTILASE FAMILY
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EMBL; L14933; AAA99906.1; -.

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LMB_HIRME
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                                                                                                                                Pfam; PF00482; P. 1.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PRODOM: PD000717; P_domain; 1.
SWART; SW00261; FU; 6.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Cleavage on pair of basic residues; Alternative splicing; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLEAVAGE (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKT5_YEAST STANDARD; PRT; 427 AA.
P36046;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 47.4 kDa protein in PASI-MST1 intergenic region.
YKL195W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76; DB 1; Length 1877;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYS-RICH MOTIF (CRM) REGION
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890955DC60534444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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                                                                           InterPro; IPR002174; Furin-like,
InterPro; IPR002884; P_domain.
InterPro; IPR000209; Peptidase_S8.
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Similarity 25.0%;
AAA87888.1;
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1877 AA;
EMBL; U47014; AAA878
PIR; B48225; B48225
HSSP; Q99405; IMPT.
                                                       808.076;
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Best Local 9
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YKT5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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  DORKKWWW CORRECT TO THE FETT T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. TENDETION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ TO TISTUCIAL 27:1-14(1995).

1. FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ TESTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING BERRYONIC DEVELOPMENT BY INTERACTING MITH OTHER EXTRACELLUAR MATRIX COMPONENTS.

2. I- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

2. I- DEVELOPMENTAL STAGE: EMBRYONIC DEVELOPMENT.

3. I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ICNHQSQRTCAA---FCRSLSCRKEQGKFYDHLLRDCISCA-SICGQHPKQCAYFCENKL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 LCRHOTRRLMASSPQFGRNSNQEKTAG----FIMGILSMAGALYFFAPNRKPLFASRKV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ESDKTAREELSSGGEQSPENEDDNNSKSDENGDDNDSKNDETEAGPØLGGDKIGASKVA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 RSPVNLPPEL----RRQRSGEVENN--SDNSGRYQGLEHRGSEASPÅLPGLKLSADQVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILNE=95370770; PubMed=7643070; Luebke A.E., Dickerson I.M., Muller K.J.; Lusbke A.E., Dickerson I.M., Muller K.J.; Lishin B-chain expression by individual glial and muscle cells in embryonic leech central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hirudo medicinalis (Medicinal leech).

Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudb.

NCBI_TaxID=6421;
                                                                                                                         Soares H.,
  haromycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 427;
                                                                                                                                                Guerreiro P., Rodrigues-Pousada C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             Maia e Silva A., Bossier P., Vilela C., Fernandes L.,
Guerreiro P., Rodrigues-Pousada C.;
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacc
                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%; Score 75.5; DB 1; 26.9%; Pred. No. 5.2; tive 20; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z28195; CAA82039.1; -.
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                                                                                            SEQUENCE FROM N.A.
                                                 NCBI_TaxID=4932;
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Best Local Simi
Matches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 GQCECPRGVTGLNCDRCDRGTY--GALPQCIPCGECFDNWDKLIAQLRDEAAAQLRIGTE 128
                                                                                                                       EMBL; U34921; AAC46862.1; -.
HSSP; P02468; IKLO.
InterPro; IPR000561; EGF-like.
InterPro; IPR000561; EGF-like.
Pfam; PF00053; Laminin_EGF.
SWART; SM00180; EGF_Lam; 2.
PROSITE; PS01022; EGF_1; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
Glycoprotein; Extracellular matrix; Repeat; Laminin EGF-like domain; Colled coil.
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LAMININ EGF-LIKE.
LAMININ EGF-LIKE.
DOMAIN II AND I.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
BY SIMILARITY.
INTERCHAIN (PROBABLE).
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

.. Database

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertebrate:* sp_mammal:*
sp_mhc:*
sp_organelle:* sp_rvirus:*
sp_bacteriap:* SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:* sp_archeap:* sp_plant:*
sp_rodent:* sp_virus:* sp_phage:* 112... 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

014836 homo sapien Q9dbz3 mus musculu Q9et35 mus musculu Q9n146 macaca mula 015030 homo sapien 015030 homo sapien Q9446 chironomus 01052 caenorhabdi Q9u241 drosophila Q9u241 drosophila Q9bxy4 homo sapien Q91108 triticum ae Oghav5 homo sapien O26489 spodoptera Description SUMMARIES Q03108 Q03107 C9DBZ3 C9ET35 Q9N146 Q96H26 015030 094446 010652 09UIF9 Q9W241 Q9BXY4 Q96K87 014836 í 10 Query Match Length DB 156 840 1704 1704 1839 1878 665 272 272 292 310 353 100.0 909 419.5 419.5 Score 140 93 93 91 89 89 88.5 86.5 86.5 86 86 Result

TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120

61

g δy QQ QΥ

121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYS¶ 166

0919m0 neoceratodu O9h8c1 homo sapien O9bgm7 homo sapien O9bgm3 homo sapien O9yb96 drosophila O9ffk8 arabidopsis Offk8 arabido		a; Euteleostomi; ae; Homo. ember of the tumor C64;	Indels 0; Gaps 0; CMSCKTICNHQSQR 60
17 85 9.4 267 13 Q919M0 18 85 9.4 1137 4 Q9H8C1 20 85 9.4 1918 4 Q9H8C1 20 83 9.4 1925 4 Q9H8C1 22 83 9.1 1925 4 Q9FFK8 23 81 9.1 1328 6 O18758 24 82.5 9.1 1328 6 O18758 25 82.5 9.1 1368 6 O18758 25 82.5 9.1 1368 6 O18751 26 82.5 9.1 1362 13 Q9EEP4 27 82 9.0 136 10 Q9EEP4 27 82 9.0 136 5 Q9YIV3 28 9.0 150 1 Q9EEP4 29 160 1 Q9EEP4 31 8.9 14	ALIGNMENTS	O	1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLG

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138 GLEHRGSEASPALPGLKLSADQVALVYST 166
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115 --PGLRLSSDQLTL-YCT 129
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Matches 76; Conservative
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 Eukaryota; Metazoa;
                  Mammalia; Eutheria;
                                                                                                                                        humoral immunity.";
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Best Local Similarity
Matches 28; Conserv
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                                NCBI_TaxID=10090;
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MEDLINE-21085660; PubMed=11217851;

A Rawal J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Radota K., Matsudi F., Suzuki R., Tomitan B., Kochiwa H.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullia M., Lee N.H.,

Ry Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyashisa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyashisa-Boris A., Yoshida K., Ramsegawa Y., Kawaji H., Kohtsuki S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
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249 AA; 26981 MW; 6F4290D719FEA037 CRC64;
                                                                                                                                                         Last sequence update)
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55.1%; Pred. No. 2.2e-39;
iive 22;, Mismatches 31;
                                                                                                                                        Created)
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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TNFRSF13B OR 120009E08RIK.
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Best Local Similarity 55.1%
Matches 76; Conservative
                                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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TNFRSF13B.
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Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 CASICGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASP 148
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Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO BROMODOMAIN ADJACENT TO ZINC FINGER DOMAIN, 2A
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01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-0c7-2000 (TrEMBLrel. 15, Last annotation update)
TRANSMEMBRANE ACTIVATOR (FRAGMENT).
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.larity 96.6%; Pred. No. 5.3e-08;
Conservative 1; Mismatches 0
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TISSUE-BRAIN;
MEDLINE-97349984; PubMed-9205841;
MEDLINE-97349984; PubMed-9205841;
MEDLINE-97349984; PubMed-9205841;
MEDLINE-97349984; PubMed-9205841;
Magase T., Ishikawa K., Nakajima D., Ohlra M., Seki N., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res 4:141-15(1997).
EMBL; AB002312; BAA20773.1; -.
InterPro; IPR001487; AT.hook.
InterPro; IPR001402; Bromodomain.
InterPro; IPR00125; DDT.
                                                                                                                                                                                                                                                                                                                                                          73 KEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC------ENKLRSPVNLPP 116
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                                                                                                                                                                                                                                                                  Gaps
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         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                10.2%; Score 93; DB 4; Length 840; 25.8%; Pred. No. 0.075; tive 17; Mismatches 68; Indels
                                                                                                                   Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008965; AAH08965.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20BBDFF1AA6BC5A1 CRC64;
                                                                                                                                                                                    3F8147D9B7034B45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           676 RGQKRKSGYSLNFSEGDGRRRRVLLRGRESPAAGP 710
                                                                                                                                                                                                                                                                                                                                                                                                                      117 ELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50014; BROMODOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1240 AA; 140417 MW;
                                                                                                                                                                                  840 AA; 94884 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02178; AT_hook; 3.
Pfam; PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00929; ATHOOK.
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00384; AT_hook; 3.
SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           015030;
01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-nFC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIAA0314 PROTEIN (FRAGMENT).
                                                                                       SEQUENCE FROM N.A.
TISSUE-LYMPH, AND LYMPHOMA;
                                                                                                                                                                                                                                                                40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02791; DDT; 1
Pfam; PF00628; PHD; 1
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
(FRAGMENT)
                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 40,
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SEQUENCE
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                                                                                                                                                    1019 KGDN---DEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTVCLAQQVEGEFTQKPGFPK 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1357 QTCPAGQSWDSQTCQCSCPATGKCTGAQFWCAKQCKCVCPVQENCKSPKVFDQTSCSCQC 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1417 PKNMQPPKGECTAGRTWDDATCTEKCATVPNCESPMVFDQATCGCKCGNKPNKLPADKVW 1476
                                                                                                                                                                                                                                      --ENKLRSPVNLPP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 -RSLSCRKEQ---GKFYDH----APF 103
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-SALIVARY GLAND;
TISSUE-SALIVARY GLAND;
Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton R.;
"Extraordinary conservation of cysteines among homologous Chironomus
                                                                                                                      -----AFCRSLSCR 72
                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Language of the control of the contr
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   Length 1240;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota, Neoptera, Endopterygota, Diptera, Nemadocera,
Chironomoidea, Chironomidae, Chironominae, Chirondmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 19, Last annotation update
                                                                                                                22 POGLWTGVAMRSCPEEQYWDPLLGTCMSCKTI - - CNHQSQRTCA
                                                                                                                                                                                                                                73 KEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                         68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 RSCPEEQYWD------PLLGTC------MSCKTICNHQ--
   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 91; DB 5;
illarity 21.4%; Pred. No. 0.28;
Conservative 22; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                              1076 RGQKRKSGYSLNFSEGDGRRRRVLLRGRESPAAGP 1110
                                                                                                                                                                                                                                                                                                                                                117 ELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151
                                                         17; Mismatches
10.2%; Score 93; 25.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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1477 CDKKCQAVCSLPPITQCPYSGQTYN 1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chironomus thummi (midge).
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 KDA SILK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 31; Conserv
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chironomoidea; Cl
NCBI_TaxID=7154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997
01-DEC-2001
                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
   Query Match
                                 Best Local
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                                                      Matches
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Eukaryota;
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                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=96003854; PubMed=7568208;
Saha V., Chaplin T., Gregorini A., Ayton P., Young B.D.;
The leukemia-associated-protein (LAP) domain, a cysteine-rich motif, is present in a wide range of proteins, including MLL, AFIO, and MLL76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 CNEERPNDAKKGACMSCNKSTCKRSFHVTCAQ-RKGLLC--EEGAI-----------172
                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 CPEEQYWDPLLGTCMSC-KTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                           5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                    Processis: 7, pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       839 AA; 89439 MW; AFBFFB9D1D35B4B8 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ZINC FINGER PROTEIN CEZF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BROWODOMAIN ADJACENT TO ZINC FINGER DOMAIN 2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 89; DB 5;
32.5%; Pred. No. 0.21;
ative 8; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1878 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILNE=20130112; PubMed=10662543;
Jones M.H., Hamana N., Nezu J., Shimane M.;
A novel family of bromodomain genes.";
Genomics 63:40-45(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AB032254; BAA89211.1; ...
InterPro; IPR001637; AT hook.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001402; DDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 CGQHPKQCAYFCENKLRSPVNLP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SRNVKYCGY-CENHLKKAINDP 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02178; AT_hook; 4
Pfam; PF00439; bromodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001739; MBD.
InterPro; IPR001965; PHD.
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                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02791; DDT; 1
Pfam; PF01429; MBD; 1
Pfam; PF00628; PHD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local, Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            proteins
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Q9UIF9
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Forns C.A., Golagne J.D.,
RA Adams M.D., Celniker S.E., Holf P.W., Hoskins R.A., Galle R.F.,
RA Gocoge R.A., Lewis S.E., Sichards S. Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandrell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Berman B.P., Bhandrari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchan P.,
Rockova D., Botchan M.R., Bouck J., Brokstein P., Botther P.,
Rockova D., Botchan M.R., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Dong Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Gabriellan A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Frosler C., Gabriellan A.E., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.M., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.M., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.M., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Wolderty B., Murphy B., Nelson M., Pitchman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R., Scheeler F., Shen H.,
Rhe Reinert K., Remington R., Stepeler R., Scheeler F., Shen H.,
Rhe Reinert K., Semington R., Stepeler R., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                        1599 PEGTTTEISYEITPRIRIWRQTLQRCRSAAHVCLCLGHLERSIAWEKSVNKVTC---- 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1653 LVCRKGDN---DEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTVCLAQQVEGEFTQKP 1709
                                                                                                                                                                                                                                                                                                                                                                                                                               LSCRKEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC-----ENKLRSPV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                         PQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTIC------NHQSQRTCAAFCRS 68
                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                  9.8%; Score 89; DB 4; Length 1878;
23.3%; Pred. No. 0.53;
tive 18; Mismatches 66; Indels
SMART: SM00384; AT_hook; 3.
SMART: SM00297; BROMO; 1.
SMART: SM00391; MBD; 1.
SMART: SM00391; MBD; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
SRQUENCE 1878 AA; 208639 MW; 12683AFE636A93A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1710 GFPKRGQKRKSGYSLNFSEGDGRRRRVLLKGRESPAAGP 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 NLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2001 (TrEMBLrel. 18, CG12489 PROTEIN.
                                                                                                                                                                                                               Ouery Match
Best Local Similarity 23.3%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neopte
Ephydroidea; Dros
NCBI_TaxID=7227;
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EMBL; X66014; CAA46812.1; -.
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CATHEPSIN B (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                 Q96KB7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q03108
Q03108;
                                                                                                                                 Q96K87
                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                   Qy
                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Walliams S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhoo Q., Zhao X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

R. The genome sequence of Drosophila melanogaster.";

R. Stance 2195 (2000).

R. EMBL; AEO03457; AAF46658.1;

R. PIYBASE; FBG0034738; CG12469.

R. InterPro; IPR001841; Znf_ring.

R. Fam: PP00373; Band_41.

SNART; SM00184; RING.

R. SNART; SM00184; RING.

R. SNART; SM00184; RING.

SNART; SM00184; RING.

SEQUENCE 665 AA; 71851 MW; D0281FBA5BA45683 CRC64;
                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                      62 CAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVN--LPPELR 119
                                                                                                                                                                                                                                                                                                                                                                                                                548 VFNPC----C------HVIA-CAQCAARCSNCPN-----CRVKITSVVKIYLPPELR 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 GVCLSSCPSGYYGTRYPDINKCTKCKADCD----TC--FNKNF-CTKCKSGFYLHLGKC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---CGOHPKQCAY--FCENKLRSPV---- 112
                                                                                                                                                                                                                                                                                                                                                          499 TGAGGSMAG---KIDLAIREKEA------REAAIERCVDTRISEAMOCK-ICMDRAINT 547
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                               2 SGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVAMRSCPEEQYWD--PLLGTCMSCKTICNHQSQRTCAAFCRSLSCRKEQGKFYDHL--- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang Yang R., Chen X., Wu C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF251057; AAK34947.1;
InterPro; IPR002174; Furin-like.

InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Busaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                      9.7%; Score 88.5; DB 5; Length 665; 25.9%; Pred. No. 0.18; ive 19; Mismatches 65; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 87; DB 4; Length 272; 24.6%; Pred. No. 0.098; ative 18; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                   65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            120 RQRSGEVENNSDNSG-----RYQGLEHRGSEASPALPGLKLSAD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAEC6B7E781189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLiel, 17, Created)
01-JUN-2001 (TrEMBLiel, 17, Last seq
01-OCT-2001 (TrEMBLiel, 18, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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272 AA; 30928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ISCASI---
                                                                                                                                                                                                                                                                                                     43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00090; tsp_1; 1.
SMART; SM00261; FU; 2.
SMART; SM00209; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50092; TSP1;
                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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THROMBOSPONDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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Best Local S
                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BXY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
Q9BXY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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74 GVCLSSCPSGYYGTRYPDINKCTKCKADCD----TC--FNKNF-CTKCKSGFYLHLGKC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | : | : | | : | 185
126 LDNCPEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGTETRVREIIQHPSA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 GVAMRSCPEEQYWD--PLLGTCMSCKTICNHQSQRTCAAFCRSLSCRKEQGKFYDHL--- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; Pooideae
Triticeae; Triticum.
NCBL_TaxID-4565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A., Hara H.,
, Takeuchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Isogai T., Ota T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H. Tanase T., Namura Y., Toqiya S., Komai F., Hara R., Takeuchi K Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AKO27346; BABS50511; -.
                                                                                                186 KGNLCPPINETRKCTVQRKKCQKGERGKKGRERKRKRPNKGESKEAIPDSK 236
                                                       113 --NLPPELRRQRSGEVENNSDNSGR--YQGLEHR-----GSEASPALPGLK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 --NLPPELRRQRSGEVENNSDNSGR--YQGLEHR-----GSEASPALPGLK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ14440 FIS, CLONE HEMBB1000915, WEAKLY SIMILAR TO
SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.2].-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bamanalia; Butheria; Primates; Catarrhini; Hominidale;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.11;
                                                                                                                                                                                                                                                        292 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 87;
24.6%; Pred. No.
tive 18; Mismatc
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(TrEMBLrel. 01, Last sequ
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"A globerellin-regulated gene from
cathepsin B of mammalian cells.";
Plant J. 2:937-948(1992).
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SEQUENCE FROM N.A.
STRAIN-VAR. CHINESE SPRING;
MEDLINE-93258430; Pubmed-1302642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                        PRELIMINARY;
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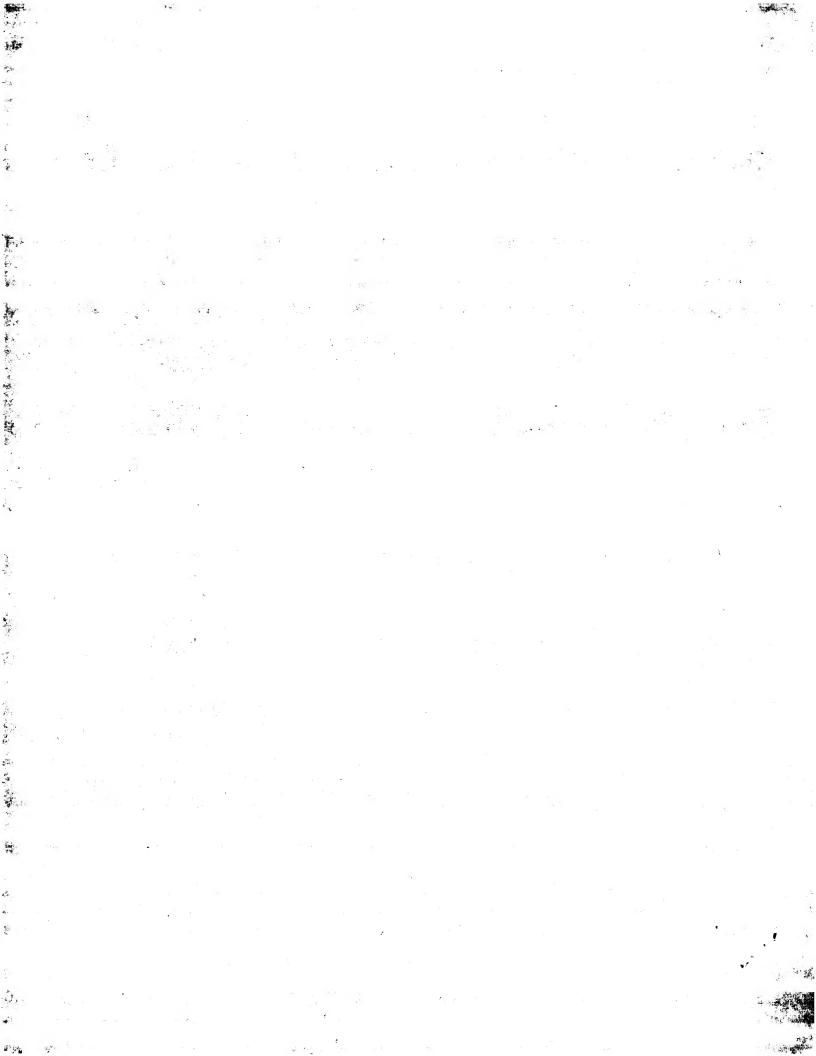
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Search completed: June 25, 2002, 16:24:30 Job time: 660 sec
                                                                                                                                                                                                                                                                               PRT;
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Best Local Similarity 22.09
Matches 26; Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE
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Q9HAV5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 KEQGKFYDHL-----LRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRRQRSGE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 ALODRFCIHLNMSVSLSVNDLLAC------CGFLCGSGCNGGYPISAWRYFRRSGV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 PQGLWTGVAMRSCPE-----EQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 PQGLWTGVAMRSCPE------EQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-VAR. CHINESE SPRING;
MEDLINE-93258430;
MEDLINE-93258430;
Dubmed-1302642;
Medline-gasts and chiney G., Baulcombe D.C.;
"A glbberellin-regulated gene from wheat with sequence homology to cathepsin B of mammalian cells.";
Plant J. 2:937-948(1992).
EMBL; X66013; CAA46811.1; -..
HSSP: P0768; 1QDQ.
                                                                                                                                                                                                                                                                                                                     9.5%; Score 86.5; DB 10; Length 310; 24.7%; Pred. No. 0.13; ative 12; Mismatches 63; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                    NÓN_TER 310 310
SEQUENCE 310 AA; 33811 MW; 2DE6F3264BB228C3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATHEPSIN B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 86.5; DB 10;
24.7%; Pred. No. 0.15;
ative 12; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 AA.
          MERORS: C01.049; -.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR00169; Thiolprot_act_site.
Pfam; PF00112; Peptidase_C1; 1.
PROSITE; PR00705; PAPAIN.
PROSITE; PS00639; THIOL_PROTEASE_CXS; 1.
Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; Papain.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 VTEECDPYFDQTGCQHPGCE--PAYP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 VENNSDNSGRYQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.7%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                      36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
HSSP; P07688; 1QDQ.
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; C01.049
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q03107
Q03107;
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MEDLINE-20495245; PubMed-11039935;
MEDLINE-20495245; PubMed-11039935;
MA TAI M., Wang L.C., Hymowitz S.C., Schilbach S., Lee J., Goddard A., de Vos A.M., Gao W.O., Dixit V.M.;
Two-amino acid molecular switch in an epithelial morphogen that if Two-amino acid molecular switch in an epithelial morphogen that regulates binding to two distinct receptors.";
Ir regulates binding to two distinct receptors.";
Science 290:523-527(2000).
REMBL, AF298812; AAC28761.1;
InterPro; IPR001368; TNFR_C6.
DR FAM: PRO0020; TNFR_C6.
SMART; SM000308; TNFR. 2.
BROSITE; PSS00652; TNFR_NGFR_1; UNKNOWN_1.
73 KEQGKFYDHL-----LRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRRQRSGE 125
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 CPEEQYWDPLLGTCMSCKTIC--NHQSQRTCA-----AFCRSLSCRKEQGKFYDHLLRD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 CISCA------SICGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVEN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 86; DB 4; Length 297; 22.0%; Pred. No. 0.14; Live 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0E71127C6C48240C CRC64;
                                                                                                                                                                                                                                                                                                                                                           Q9HAV5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
x-LINKED ECTODYSPLASIN-A2 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                  297 AA
                                                                                                                                                       126 VENNSDNSGRYQGLEHRGSEASPALP 151
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 25, 2002, 16:16:08; Search time 88.08 Seconds (without alignments) 209.335 Million cell updates/sec Run on:

US-09-854-864-15 909 . 1 MSGLGRSRRGGRSRVDQEER.....SPALPGLKLSADQVALVYST 166 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1985.DAT:*
6: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1980.DAT:*
8: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1980.DAT:*
9: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1980.DAT:*
110: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1991.DAT:*
111: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1991.DAT:*
112: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
113: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
114: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
115: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1998.DAT:*
116: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
117: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
118: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
119: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
120: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
121: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
122: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
123: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
124: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
125: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
126: /SIDSI/gogdata/geneseq/geneseqp-embl/AA1999.DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human lymphocyte s	Human TACI splice	Human lymphocyte s	Human neutrokine-a	A transmembrane ac	Human TACI protein	Human tumour necro	Human BR43x2, an i	A murine ztnf4, a	Human TANGO 140-2.	Human polypeptide
SUMMARIES	Ω	AAW75785	AAE09244	FAW75783	AAB36312	AAY94000	AAE09240	AAY71914	AAY93998	FAY 94 006	AAB01421	AAM42025
		19	22	19	21	21	22	22	21	21	21	22
	Query Match Length DB	166	265	293	293	293	293	293	247	249	197	1589
œ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	62.8	46.1	10.5	10.2
	Score	606	606	606	606	606	606	606	599	419.5	95	93
	Result No.	п	7	٣	4		9	7	æ	6	10	11

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(GETH ) GENENTECH INC.
                                                                WPI; 2001-541628/60.
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                   265 AA;
                            Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-1999
                                                                                                                                antagonists
                                                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local S
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                                         Yan M;
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                                                                                 This is the amino acid sequence of the N-terminal, i.e. the extracellular, domain of novel human transmembrane activator and extracellular, domain of novel human transmembrane activator and cartracellular, domain of novel human transmembrane activator and matcheractor (TACI) protein (see AAM75783). TACI is a lymphocytes and to a much lesser extent it is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. The extracellular domain of TACI functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the C-terminal portion (see AAM75784) of TACI to the N-terminal domain of CAMI. A recombinant form of the extracellular portion of TACI acts as a dominant-negative or blocking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TACI, in which binding of a candidate molecule is determined by detecting cellular activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                                                                                                                                                                                                                                                                                                                      Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 909; DB 19;
100.0%; Pred. No. 2.3e-83;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE09244 standard; Protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TACI splice variant protein.
                                                             Claim 8; Page 73; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2000; 2000WO-US32378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0182938
2000US-0226986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                   Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200160397-A1.
  New isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 FEB-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE09244;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                        disease
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61 TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
   Pitti RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCWA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCWA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, proclassis and lupus erythematosus. The present sequence is human
                                                                                                                                                         Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium signal-modulating cyclophilin ligand; human; hyphocyte surface receptor; human; B-cell; B lymphocyte; lifection; cancer; rheumatoid atthritis; autoimmune disease; glomerulonephritis; immunosuppressive; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 265;
Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACI; transmembrane activator and CAML-interactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 909; DB 22 100.0%; Pred. No. 4.1e-83
   Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Transmembrane_domain
187..294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Grewal I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Example 1; Fig 6; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW75783 standard; Protein; 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant rejection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rACI splice variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Dodge KH,
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(first entry)

26-FEB-2001

AAB36312;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated transmembrane activator protein - used to develop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of novel human transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 909; DB 19;
100.0%; Pred. No. 4.6e-83;
ive 0; Mismatches 0;
/label= Cytoplasmic_domain
/note= "Claim 6"
34..71
                                                                                                "TNFR_NGFR motif"
                                                                                                                                                                                                                                                                                                                                                                                                                              (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Fig 2a; 89pp; English.
                                                                                                                                                                                                                                                                                            98WO-US04270.
                                                                                                                                                                                                                                                                                                                                                             97US-0810572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            graft versus host disease.
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Matches 166; Conservative
                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Von Bulow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-506346/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV57328
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                                                                                                                                                                 WO9839361-A1
                                                                                                                                                                                                                                                                                            03-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1997;
                                                                                                                                                                                                                              11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bram RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease
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AAB36312 standard; Protein; 293 AA.

RESULT
AAB36312
ID AAB3

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                                                                                                             Human; neutrokine-alpha binding protein; NAR protein; TR17; cytostatic; immunosuppressive; nootropic; neuroprotective; antivital; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antidicer; cardiant; ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders and autoimmune disorders. The TR17 polypeptides, polynucleotides, antibodies, agonists and/or antagonists are used for treating various other diseases defined in the specification and as research tools for studying the phenotypic effects that result from inhibiting TR17/TR17 ligand interactions on various cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding a neutrokine-alpha receptor (NAR) such as TRI7, useful for producing TRI7 protein which is used in the treatment and diagnosis of autoimmune and immunodeficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ndels
                                                                               4uman neutrokine-alpha binding protein TR17 SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 msglgrsrrggrsrvdgeerfpgglwtgvamrscpeegywdpllg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 909; DB 21;
100.0%; Pred. No. 4.6e-83;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Ullrich S, Baker K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 1; Fig 1; 398pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                               26-MAR-1999; 99US-0126599.
10-MAR-2000; 2000US-0188208.
                                                                                                                                                                                                                                                                                                                24-MAR-2000; 2000WO-US07966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-602359/57.
                                                                                                                                                                                 autoimmune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC64602
                                                                                                                                                                                                                                               WO200058362-A1.
                                                                                                                                                                                                                  Homo sapiens
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ID AAY94
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121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166

AAE09240 standard; Protein; 293 AA

AAE09240

(first entry)

19-NOV-2001

AAE09240;

Human TACI protein.

Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis;

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The present sequence represents a human transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TACI) receptor. TACI is a tumour necrosis factor (TAE) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The rutibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthemia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA ceceptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, is emphysema, end stage renal failure, glomerulonephritis, vasculitis, is the chain receptor-ligand engagement is enablasms, multiple myelomas, lymphomas, lymth chain receptor-ligand engagement and receptor-ligand engagement and receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, is the chain receptor-ligand engagement and receptor-ligand enga
                                                                                                                                                                                                                          transmembrane activator and CAML-interactor; tumour necrosis factor; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; wasculitis; nephritis; repail neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          light chain neuropathy, anyloidosis, moderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agoniëts or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and
                                                                                                                                                                                              Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                              A transmembrane activator and CAML-interactor (TACI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 149-150; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yee DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JAN-2000; 2000WO-US00396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholesterol or renal emboli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0226533
                                                             20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-452538/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200040716-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-2000.
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Marsters SA, Pitti RM;

Grewal I, Kim KJ,

Ashkenazi AJ, Dodge KH,

Yan M;

WPI; 2001-541628/60.

N-PSDB; AAD15901

(GETH) GENENTECH INC

28-NOV-2000; 2000WO-US32378.

WO200160397-A1. Homo sapiens.

psoriasis.

23-AUG-2001

2000US-0182938. 2000US-0226986.

16-FEB-2000; 22-AUG-2000;

Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or

Example 1; Fig 1; 160pp; English.

antagonists

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The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of FNF (tumour necrosis factor) especially TALL-1. APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              They are useful for treating a mammal suffering from cancer such as leukaemia. Imphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 909; DB 22; 100.0%; Pred. No. 4.6e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rACI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Best Local 8
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Gaps

1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60

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*1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60

100.0%; Score 909; DB 21; 100.0%; Pred. No. 4.6e-83; ive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 166; Conservative

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Gaps

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Length 293; Indels us-09-854-864-15.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein. TACI (Transmembrane activator and calcium-signal modulating protein. TACI (Transmembrane activator and calcium-signal modulating alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L complex is useful for modulating an intracellular signalling cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are used to inhibit the interaction between TACI and TACI-L for therapeutic purposes to treat tumnour and tumnour metastasis and to combat various autoinmune diseases e.g. multiple sclerosis and diabetes, as well as other disorders, such as viral infection, rheumatoid arthritis, and inflammation. The interaction is used to study cellular processes associated with tumnour necrosis factor (TNF)-receptors such as immune required to the compation, cell proliferation, cell death and inflammatory responses.
                                                                                                                                                                                                                                                                                   tumour necrosis factor receptor; TNF; autoimmune disease; dlabetes; calcium-signal modulating cyclophilin ilgand; CAML; viral infection; neutrokine alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy; neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour; antiarthitic; antirheumatic; immunosuppressive; multiple sclerosis; rheumatoid arthritis; graft rejection; inflammation; cell proliferation; cell death; immunoglobulin E-mediated allergic reaction; IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Binds with amino acids 123-285 of extracellular domain of TACI-L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of new interactions between tumour necrosis factor receptors (TACI) and TACI ligands to screen candidate molecules for determining agonist and antagonist interactions which are used for treating inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a human tumour necrosis factor receptor (TACI)
                        1 msglgrsrrggrsrvdgeerfpgglwtgvamrscpeegywdpllgtcmsckticnhqsgr 60
                                                                                                                                                                                                                                                                     Human; transmembrane activator and CAML interactor; TACI;
                                                                                        QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                Human tumour necrosis factor receptor (TACI) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         'label- Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                      A
                                                                                                                                                                  AAY71914 standard; Protein; 293
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                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Din WS;
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N-PSDB; AAD02006.
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin RG,
                                                                                                                                                                                                                     26-MAR-2001
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                                                                                                                                                                                            AAY71914;
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  f TACI and TACI-L can
cell types TACI-L
                                                                                                                                                                                                                                                                                                                                                                   TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCHNKLRSPVNLPPELRR 120
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   TCMSCKTICNHQSQR 60
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                            Length 293;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pseudo repea
The interaction between the extracellular region of be used to further develop understanding of which
                                                                                                                                                                                                                                                   1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLG
                                                                                                                                                                                                      ó
                                                                                                                                                                                 Pred. No. 4.6e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BR43x2, an isoform of the TACI receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "transmembrane domain"
134..247
/note= "cytoplasmic domain"
                                                                                                                                                            DB
                                                                                                                                                                                                      Mismatches
                                                                                                                                                          100.0%; Score 909;
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/note= "cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY93998 standard; Protein; 247
                                                                                                                                                                                                      ;
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                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37-JAN-2000; 2000WO-US00396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                 Similarity
                                                                                        293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA58556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200040716-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1999;
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                                                                                                                                                                                                      Matches 166;
                                                 acts upon
                                                                                           Sequence
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93998
                                                                                                                                                                                    Best Local
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Jomain
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ID AAY9
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13-JUL-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
             renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPELRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 msglgrsrrqgrsrvdqeer----- 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 -----slscrkeggkfydhllrdciscasicgghpkqcayfcenklrspvnlppelrr 74
Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 599; DB 21; Length 247;
Pred. No. 4.7e-52;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine ztnf4, a tumour necrosis factor ligand.
                                                     Claim 62; Page 145; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY94006 standard; Protein; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  65.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                               72.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.3
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        247 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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WO200040716-A2.

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The present sequence represents murine ztnf4, a tumour necrosis factor ligand. The extracellular domains of BR43x2 (an isoform of the cransmenbrane activator and CAML-Interactor (TACI) receptor). TACI or ECCH (a related B cell protein) contain a cysteine rich domain, and are used for inhibiting ERASA; ARCI or ECCHA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autibody production. The antibody production is associated with an autibody production. The antibody production is associated with an autibody production. The antibody production is associated with a subtimule disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The zinf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with a sthma. Dronchitis, emphysems, end stage renal failure, capture, and erating immune response, immunosuppression, graft capture, and erating immune response, inflammation, insulin dependent diabetes mellitus, Crohn's disease, inflammation, insulin dependent capture shork. BR43x2, TACI, and BCMA polypeptides, fusulos, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli.
                                                                                                                                                                                                                                                                                         renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 CASICGOHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 VAMRSCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCIS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.1%; Score 419.5; DB 2.55.1%; Pred. No. 4.8e-34; Live 22; Mismatches 31
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 163; 175pp; English.
                                                                                                                                                                        Yee DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB01421 standard; Protein; 197 AA.
                                                      07-JAN-2000; 2000WO-US00396
                                                                                           99US-0226533
                                                                                                                                                                        Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 ALPGLKLSADQVALVYST 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                            WPI; 2000-452538/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TANGO 140-2.
                                                                                                                                                                        Xu W,
                                                                                                                                                                                                                                N-PSDB; AAA58566
                                                                                           07-JAN-1999;
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                                                                                                                                                                        Gross JA,
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22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postnasis, inflammatory bowel disease, septic shock, ulcerative colitis, conn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chiseases e.g. myasthemia cancer, liver diseases, cachexia and autoimmune diseases e.g. myasthemia acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are sultable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 YDHLLRDCISCA-----SICGQHPKQCAYFCENKLRSPVNLPPELRRQRS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tglptmdcqeneywdq-wgrcvtcqr-cgpgqelskdcgygeggdayctacpprrykssw 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGVAMRSCPEEQYWDPLLGTCMSCKTIC -- NHQSQRTCA -- -- AFCRSLSCRKEQGKF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 95; DB 21; Length 197; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
                                                                                                                   prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular disorders can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM42025 standard; Protein; 1589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 3; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
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                                                                                                                                                                                                                                                                                                               99WO-US31025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-465743/40.
N-PSDB; AAA47454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197
                                                                                                                                                                                                               WO200039284-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              991qd 123
                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                            23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                           30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holtzman DA;
                                                                                                                                                                                                                                                                06-JUL-2000
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Best Local S:
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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AAM42025
    WALKER WANKER WALKER WANKER WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin, Inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pegttteisyeitprirvwrqtlercrsaaqvclclgqlersiaweksvnkvtc--lvcr 1325
                                                     gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ENKLRSPVNLPP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral sclerosis; shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AFCRSLSCR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
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Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 KEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 6956; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.5;
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Human polypeptide SEQ ID NO 6956.
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Wehrman T, Xu
Goodrich R,
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2000US-052317.
2000US-0598042.
2000US-06581450.
2000US-06531450.
2000US-06531450.
2000US-0633036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, A
Wang Z, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                      Homo sapiens.
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19-OCT-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                   leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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7;

Gaps

30;

68; Indels

25.8%; Pred. No. 2.7; ive 17; Mismatches

40; Conservative

22 POGLWTGVAMRSCPEEQYWDPLLGTCMSCKTI--CNHQSQRTCA-----AFCRSLSCR 72

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(first entry)

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1506 kgdn---defillcdgcdrgchiychrpkmeavpegdwfctvclagqvegeftgkpgfpk 1562
                                                                                            1448 pegttteisyeitprirvwrgtlercrsaagvclclgglersiaweksvnkvtc--lvcr 1505
                                                                                                                                73 KEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC-----ENKLRSPVNLPP 116
                                                                                                                                                                                                                                  117 ELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 3384.
                                                                                                                                                                                                                                                                                                                                                 AAM40239 standard; Protein; 1878
Best Local Similarity
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                  Matches
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[ull-length cDNAs defined in the specification. Where a primer set
complaises: (a) an oligo-dT primer and an oligonuclectide complementary
to the complementary strand of a polynuclectide comprises one of
the 5602 nucleotide sequences defined in the specification, where the
cligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence of the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
clin end of diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03165 to AAH13628 and
AAH13633 to AAH13642 represent human anino acid sequences; and AAH13629 to AAH13632
represent child, and of the abnormality of the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagal K,
                                      1383 rgqkrksgyslnfsegdgrrrrvllrgrespaagp 1417
                117 ELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nıkawa T, Hayashi K,
Wakamatsu A, Naqai K
                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:18183
                                                                                                                                                  AAB95554 standard; Protein; 1727 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isoqai T,
                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang D;
immunosuppressant; cytostatic; gene therapy; cancer;
                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hamenstatic; Alzheimer's; Parkinson's disease; hamenstatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemotactic; chemotactic; chemotactic; chemotactic; diseases as screening; arthritis; inflammation;
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Zhang J;
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Yang Y,
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Wehrman T, Xu
Goodrich R,
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2000US-0598042.
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2000US-0662191.
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N-PSDB; AAI59395.
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Wang Z,
Human; nootropic;
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09-JUL-2000;
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                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                  leukaemia.
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Wang J,
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utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                             Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                 1599 pegttteisyeitprirvwrqtlercrsaaqvclclgqlersiaweksvnkvtc--lvcr 1656
                                                                                                                                                                                                                                                                  1657 kgdn---defillcdgcdrgchiychrpkmeavpegdwfctvclaqqvegeftqkpgfpk 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D;
                                                                                                                                                                                                                                         73 KEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC-----ENKLRSPVNLPP 116
                                                                                                                                                                                         POGLWTGVAMRSCPEEQYWDPLLGTCMSCKTI--CNHQSQRTCA-----AFCRSLSCR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hautington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
                                                                                                                                                                   30;
                                                                                                                                          DB 22; Length 1878;
                                                                                                                                        ch 10.2%; Score 93; DB 22; Length 187. Similarity 25.8%; Pred. No. 3; 40; Conservative 17; Mismatches 68; Indels
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Yang Y,
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Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                           117 ELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151
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                                                                                                                                                                                                                                                                                                                                                                                AAM39716 standard; Protein; 266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2861.
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Wehrman T, Xu
Goodrich R,
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25-APK-2000; 2000US-0552317.
09-UUL-2000; 2000US-058042.
19-UUL-2000; 2000US-0620312.
03-AUC-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; AAI58872.
                                                                                                     1878 AA;
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Wang Z,
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                                                  C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200153312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eukaemia.
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Wang J, Wang Zhao QA,
                                                                                                      Sednence
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Best Local $
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                               The invention relates to human nucleic acids (AAIS)798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with hootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinhibin activity, chemotactic/chemokinetic lactivity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, as assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional regulator; transcription; BAZ1-alpha; bromodomain; BAZ; atypical zinc finger; testis; human; tumour; BAZ1-beta; BAZ2-alpha; drug; BAZ2-beta; treatment; cancer; proliferative disorder; screening.
                                                                                                                                                                                                                                                                104 CENKLRSPVNLP------PELRRQRSGE----VENNSDNSGRYQG-LEHRGSE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 266; 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Example 4; SEQ ID NO 2861; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB 2
Pred. No. 0.37;
25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                   10.18;
24.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 46; Conservat
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252 sskslpnfpi 261
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18-APR-1997;
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This sequence represents the human BAZ2-alpha protein, a member of a family of transcriptional regulator genes containing a bromodomain (BAZ, Bromodomain with Atypical Zinc finger) which are expressed specifically in testis tissue and also in certain tumour lines. Transgenic cells may be used for the preparation of the BAZ1-alpha, BAZ1-beta, BAZ2-alpha and BAZ2-beta proteins. These proteins can be used in the treatment of cancer and other proliferative disorders, and in screening of compounds for their binding ability to the expression products (e.g. for use as drugs by modulation of transcriptional regulation).
                                                                    Transcriptional regulator gene family containing bromodomain - may
be expressed in testis tissue and is useful for treatment of cancer
and other proliferative disorders
                                                                                                                                                                  Claim 1; Page 72-88; 187pp; Japanese.
WPI; 1998-583603/49.
N-PSDB; AAV68396.
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Sequence 1878 AA;

9 1599 pegttteisyeitpririwrqtlqrcrsaahvclclghlersiaweksvnkvtc----- 1652 1653 lvcrkgdn---deflllcdgcdrgchiychrpkmeavpegdwfctvclaqqvegeftgkp 1709 69 LSCRKEQGKFYDHLLRDCISCASICG---QHPKQCA----YFC-----ENKLRSPV 112 Gaps 22 PQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTIC------NHQSQRTCAAFCRS 68 38; Query Match 9.8%; Score 89; DB 19; Length 1878; Best Local Similarity 23.3%; Pred. No. 7.5; Matches 37; Conservative 18; Mismatches 66; Indels 31 113 NLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPALP 151 g οy a ò ó

Search completed: June 25, 2002, 16:16:09 Job time: 289 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 25, 2002, 16:22:44; Search time 27.55 Seconds (without alignments) 94.164 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-854-864-16 405 1 CPEEQYWDPLLGTCMSCKTI......DCISCASICGQHPKQCAYFC 67

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	915 homo sapie	mus m	P29122 homo sapien	bos t	P30432 drosophila		mus n	Q92824 homo sapien	mus n	Q62799 rattus norv	P19137 mus musculu	mus n	рошо		felis	Q63415 rattus norv	093571 ictalurus p	Q02858 mus musculu		P51902 gadus morhu	-	P04412 drosophila	P49134 rattus norv	_	Q9nj15 branchiosto	P41413 rattus norv	Q61789 mus musculu	s mus	_		ď	2 haem	Q06807 bos taurus
SUMMARIES	CII	19	PCK5_MOUSE	PAC4_HUMAN	ITB1_BOVIN	FUR2_DROME	TIE2_HUMAN	ITB1_MOUSE	PCK5_HUMAN	TRA2_MOUSE	ERB3_RAT	LMA1_MOUSE	EGFR_MOUSE		TR17_HUMAN	ITB1_FELCA	PAC4_RAT	MT_ICTPU	TIEZ_MOUSE	EGFR_HUMAN	MTGADMO	VEGD_MOUSE	EGFR_DROME	ITB1_RAT	ERB3_HUMAN	PCK5_BRACL	PCK5_RAT	LMA3_MOUSE	LMA2_MOUSE	FBL4_MOUSE	ITB1_XENLA	ECLH_DROME	ANTA_HAEGH	TIEZ_BOVIN
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	5 63.5 15.7 388 1 6 63.5 15.7 400 1 7 63 15.6 474 1 6 21.5 15.4 619 1 6 2.5 15.4 619 1 6 2.5 15.4 388 1 6 2.5 15.4 417 1 6 2.5 15.4 798 1	ALIGNMENTS	ULT 1 VECD_HUMAN VECD_HUMAN O43915; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Vascular endothelial growth factor D precursor growth factor) (FIGF).	FIGE ON VEGED. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBL_TaxID=9606;	SEQUENCE FROM N.A. TISSUE-Lung; MEDLINE=97349118; PubMed=9205122; MEDLINE=17, Nezu JI., Shimane M., Hir "Molecular cloning of a novel vascular VEGF-D."; Genomics 42:483-488(1997).	SEQUENCE FROM N.A. TISSUE-Lung; MEDLINE-98140120; PubMed-9479493; MCChigiani M., Lestingi M., Luddi A., Orlandini Rossi E., Ballabio A., Zuffardi O., Oliviero S.; "Human FIGF: cloning, gene structure, and mapping between the PIGA and the GRPR genes.";	MEDLINE-98118549; PubMed-9435229; MEDLINE-98118549; PubMed-9435229; Achen M.G., Jacker S.A.; Alitalo K., Stacker S.A.; "Vascular endothelial growth factor D (VEGF-D) is tyrosine kinases VEGF receptor 2 (FIK1) and VEGF "Froc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).	PROCESSING, AND SEQUENCE OF 89-94; 100-10 MEDLINE-20011413; PubMed-10542248; Stacker S.A., Stenvers K.L., Caesar C., v Stacker S.A., Stenvers K.L., Caesar C., v Nice E.C., Roufail S., Simpson R.J., Morialo K., Achen M.G.; Alitalo K., Achen M.G.; Pibson R.J., Morialo K., Achen M.G.; Proteolytic processing which generates no J. Balol. Chem. 274:32127-32136(1999). -! FUNCTION: Growth factor active in ang and endothelial cell growth, stimulate migration and also has effects on the vessels. May function in the formatic vascular systems during embryogenesis of differentiated lymphatic endothelial activates VEGFR-2 (FIk1) and VEGFR-3

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Nakayama K.
                                                                          PCK5_MOUSE
                           RESULT 2
PCK5_MOUSE
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGFR-1 is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interaction.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Highly expressed in lung, heart, small intestine and fetal lung, and at lower levels in skeletal muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV-CKTPCPKD 280
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                                                                       colon, and pancreas.
PTM: Undergoes a complex proteolytic maturation which generates
                                                                                                                                                                                                               bound by non-covalent interactions.
SIMILARITY: BELONGS TO THE PDGE/VEGF FAMILY OF GROWTH FACTORS.
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1 (APPROXIMATE).
3.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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RISSP, 1915692; 1VPP.

R Dries, PP00341, PDGF; 1.

R ProDom; PD001629; PDGF; 1.

R PRART; SM00141; PDGF; 1.

R PROSITE: PS00249; PDGF-1; 1.

R PROSITE; PS50278; PDGF-2; 1.

R Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Witogen; Growth factor; Glycoprotein; Signal; Repeat; Mitogen; Growth factor; Glycoprotein; Mitogen; Mitogen
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INTRACHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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EMBL, Y12863, CAA73370.1, -
EMBL, Y12864, CAA73371.1, -
EMBL, Y12865, CAA73371.1, JOINED.
EMBL, Y12866, CAA73371.1, JOINED.
EMBL, Y12867, CAA73371.1, JOINED.
EMBL, Y12868, CAA73371.1, JOINED.
EMBL, Y1289, CAA73371.1, JOINED.
EMBL, Y12870, CAA73371.1, JOINED.
EMBL, X128010185, CAA03371.1, JOINED.
EMBL, AJ00185, CAA03942.1, -
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354 AA;
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Matches 28; Conserv
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Rancourt S.L., Rancourt D.E.;
"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, sonitogenesis, and skeletal formation.";

Jerost 21:75-81(1997)

Pev. Genet. 21:75-81(1997)

Per UNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION OF GROWTH FACTORS.
               004592; 062040; 01-FEB-1995 (Rel. 31, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Proprotein convertase subtilisin/Kexin type 5 precursor (EC 3.4.21.-) (Proprotein convertase PC5) (Subtilisin/Kexin-like protease PC5) (Convertase PC5) (Subtilisin/Rexin-like protease PC5)
                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa T., Murakami K., Nakayama K.; "Identification of an isoform with an extremely large Cys-rich region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL EXPRESSION.
MEDLINE=96293359; PubMed=8698813;
Constam D.B., Calfon M., Robertson E.J.;
"SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenes1s.";
J. Cell Biol. 134:181-191(1996).
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MEDLINE-93342056; PubMed-B341687;
MEDLINE-93342056; PubMed-B341687;
MEDLINE-93342056; PubMed-B341687;
MEDLINE-93342056; PubMed-B341687;
Causon J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/kexin-like Pc5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97103178; PubMed-8947550; De Ble I., Marchiklewicz M., Malide D., Lazure C., Nakayama K., Bendayan M., Seidah N.G.; "The isoforms of proprotein convertase PC5 are sorted to different "The isoforms of proprotein
                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mammalian Kex2-11ke processing endoprotease family: its striking structural similarity to PACE4."; J. Biochem. 113:132-135(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification and functional expression of a new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                           of PC6, a Kex2-like processing endoprotease.";
FEBS Lett. 327:165-171(1993).
                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).
  1877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM PC5A).
TISSUE-Brain, and Intestine;
MEDLINE-93224489; PubMed-8468318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM PC5A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell Biol. 135:1261-1275(1996).
                                                                                                                                                                                                                                                                                                                                       STRAIN-ICR; TISSUE-Intestine;
MEDLINE-93327934; PubMed-8335106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL EXPRESSION.
MEDLINE-97436919; Pubmed-9291583;
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                  AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.

-1 TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST ABUDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE MUDANT IN THE INTESTINE AND LOWE BUT NOT IN THE BRAIN.

-1 DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO, EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER, BUT WARKEDIX UPREGULATED A DISCRETE SITES DURING DEVELOPMENT. AT E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENCIATED DECIDUA. AT E7.5, INTERNE EXPRESSION IN EXTRABUBRYONIC ENDODERW, ANNION AND NASCENT MESODERW. AT 8.5, ABUDANT EXPRESSION IN SOMITES AND YOLK SAC FOLLOWED BY A CONFINATION TO DERMANOTOME COMPARTMENT. BETWEEN E9.5 AND E11.5, ABUDANT EXPRESSION IN THE LIMBS IS CONFINED COLLOWER SERVED. OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED STAGE. STRONG BESENCHINK SURROUNDING THE CARTILAGE. AT THIS STAGE. STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
                                                                                                                                                                                                                                                                                                                                                                                           CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI. STOOFDAM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF DOMAIN: THE PROPEPTIED DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
                  CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
SUBCELLUIALB LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS WITH THE TGN SORTING PROTEIN PACS-1.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                       ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00723; SUBTILISIN.
Prodom; PD000717; P_domain; 1.
Prodom; PD000717; P_domain; 1.
SWART; SW00181; EGF; 3.
SWART; SW00261; FU; 22.
SWART; SW00261; FU; 22.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00139; SUBTILASE_HIS; 1.
PROSITE; PS00139; SUBTILASE_HIS; 1.
PROSITE; PS00139; SUBTILASE_SIR; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Cleavage on pair of basic residues; Repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002884; P_domain.
InterPro; IPR000209; Peptidase_S8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000561; EGF-like.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D17583; BAA04507.1; -.
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116
1877
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PIR; A48225; A48225.
HSSP; Q99405; 1MPT.
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                                                                                    EARLY ENDOSOMES
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SPTQEDCISCPVTRVLD ->
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P29122; 015099; 005100; 090EJT; 090EJT; 090EJT; 090EJT; 090EGT; 094KG9; 094KH0; 094KH1; 010EC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1001 (Rel. 40, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin|like proprotein
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(BY SIMILARITY).
(BY SIMILARITY).
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(POTENTIAL).
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                                                                                                                                SIMILARITY).
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                                                                                 CYS-RICH MOTIF (CRM) REGION
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EXTRACELLULAR (POTENTIAL).
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                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                             CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY N-LINKED (GLCNAC...))
N-LINKED (GLCNAC...)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                               AC 1.
AC 2.
CLEAVAGE (AUTO-) (BY S
CELL ATTACHMENT SITE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EC850E2DF20EA1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Identification of a second human subtilisin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E.,
                                                                                                                                                              CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
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SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN ISOFORM PC5A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 1;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.8;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1538 KDSQQCVLCHSSCRTCEGPHSMQC 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; PubMed=1741956;
                                                                 HOMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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25.0%;
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1877 AA; 209287
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Best Local Similarity 25.0°
Marches 21, Conservative
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ACT_SITE
ACT_SITE
CARBOHYD
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SEQUENCE
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us-09-854-864-16.rsp

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MEDLINE-97335942; PubMed-9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
"A novel human PACE4 isoform, PACE4E is an active processing protease
containing a hydrophobic cluster at the carboxy terminus.";
J. Blochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; Genomic organization and alternative splicing of human PACE4 (SPC4), kexin-like processing endoprotease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Blochem. J. 339:639-647(1999).
                                                       "Identification of novel cDNAs encoding human kexin-like protease, PACE4 isoforms.";
                                                                                                                                                                       "Identification of novel cDNAs encoding human kexin-like protease,
                         Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
                                                                                                                                              Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                           Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A., Matsuda Y.;
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SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
MEDLINE=98021085; PubMed=9378725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97064242; PubMed-8906861; Seidah N.G.; Senorg M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; Eunctional analysis of human PACE4 A and PACE4-C isoforms: identification of a new PACE4-CS isoform.;
                                                                                                                                                                                                                                                                                      "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                    [5]
SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                   Biochem. Blophys. Res. Commun. 204:1381-1382(1994)
                                                                                     Biochem. Biophys. Res. Commun. 200:943-950(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING (ISOFORM PACE4CS).
                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99233559; PubMed=10215603;
             MEDLINE=94235049; PubMed=8179631;
                                                                                                                            MEDLINE-95071480; PubMed-7980617;

    Biochem. 122:438-452(1997).

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                                                                                                                                                                                                                                                                                                                                                TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                      PACE4 isoforms.";
                                                                                                                                                                                                                                               TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moehring T.J.
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                                                                                                                 ERRATUM
                                                                                                                                                          Matsuda
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JOINED. JOINED. JOINED.

BAA21620.1; BAA21620.1;

BAA21620. BAA21620. BAA21620. BAA21621. BAA21621.

AB001900; AB001901; AB001902; AB001903;

EMBL; EMBL;

BAA21620.1; JOINED BAA21620.1; JOINED

EMBL; M80482; AAA59998.1; -. AB001914; BAA21620.1; AB001898; BAA21620.1; JOINED.

AB001904;

EMBL; EMBL; EMBL; EMBL; JOINED JOINED

BAA21621

AB001914; AB001898; AB001901; AB001902; AB001904;

EMBL;

EMBL;

EMBL; EMBL; EMBL: EMBL; EMBL; EMBL;

JOINED. JOINED. JOINED. JOINED.

BAA21621.

EMBL;

BAA21621 BAA21621 BAA21621 BAA21621 BAA21621 BAA21621 BAA21621

JOINED. JOINED.

AB001906; AB001907;

JOINED. JOINED.

> AB001906; AB001908;

JOINED

JOINED.

BAA21622 BAA21622 BAA21622 BAA21622 BAA21622 BAA21622 BAA21623

EMBL;

JOINED

BAA21622 BAA21622

AB001909;

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EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

BAA21622 BAA21621

JOINED. JOINED.

> BAA21623 BAA21623

EMBL; EMBL;

EMBL: EMBL; BAA21623.1;

BAA21623

AB001905; AB001906;

EMBL;

WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT

EMBL;

JOINED JOINED

BAA21623

EMBL;

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TERMINUS. PACE4 MIGHT BE SECRETED.

-1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; PACE4A-I/PACE4 (SHOWN HERE),
PACE4A-II, PACE4, PACE41, PACE4C., PACE4CS, PACE4CS, PACE4D.)
PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
-1- TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA, PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CERRBELLOM,
PLACENTA AND PITUITARY. PACE4E-I IS SYPRESSED IN CERRBELLOM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             SUBCELLULAR LOCATION: PACEGA-I AND PACEGA-II ARE SECRETED. PACEGC AND PACEGCS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM IN ENDOPLASMIC RETICULUM. PACEGE-I AND PACEGE-II ARE RETAINED INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
                                                                                                                                                                                                                                                                                                                      CEREBELLUM.

DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOSORW PACEAU LACKS THE PROPEPTIDE DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILLASE FAMILY.
 PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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us-09-854-864-16.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its dontent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
FOR VCAM1 AND RECOGNIZES THE SEQUENCE 0-1-D-S IN VCAM1. INTEGRIN ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND OSTEDOPNIN. IT RECOGNIZES THE SEQUENCE A-E-1-D-G-T-E-L IN CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPILIGRIN AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A SUBDINIT: HETERODIMEN OF AN ALPHA AND A BETA SUBUNIT. BETA-1 ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM BETA-1B DOES NOT LOCALIZE TO FOCAL ADHESIONS.
-!- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U10865; AAA80571.1; -.

R InterPro; IPR000561; EGF-like.

R InterPro; IPR001369; Integrin_B.

InterPro; IPR001369; Integrin_B.

R InterPro; IPR001811; Integrin_B: 1.

Prodom; PD001811; Integrin_B; 1.

R SMART; SM0001; EGF_like; 1.

SMART; SM0001; EGF_like; 1.

SMART; SM00423; PS1; 1.

R PROSITE; PS000423; PS1; 1.

R PROSITE; PS000423; EGF_l; UNKNOWN_2.

R PROSITE; PS00042; EGF_l; UNKNOWN_2.

Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; R Repeat; Phosphorylation.

I DOMAIN <1 705 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                      -:- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
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DOMAIN
      WEDLINE-95399478; PubMed=7545439;
Waclaren L.A., Wildeman A.G.;
Maclaren L.A., Wildeman A.G.;
"Fibronectin receptors in preimplantation development: cloning,
"Fibronectin receptors in preimplantation development: cloning,
"Fibronectin receptors in preimplantation development: cloning,
"This of the alpha 5 and beta 1 integrin
RT aubunits in bovine trophoblast.";
Biol. Reprod. 53:153-165(1955).
C-1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-1/BETA-1 AND ALPHA-2/BETA-1, ALPHA-3/BETA-1, ALPHA-3/BETA-1, ALPHA-4/BETA-1, ALPHA-
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 969:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin beta-1 (Fibronectin receptor beta subunit) (CD29)
(Integrin VLA-4 beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
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Pred. No. 1.2;
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BAA21624.1;
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BAA21624.1;
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NCBI_TaxID=9913;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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P53712;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
10 X TANDEM REPEATS, CYS-RICH.
                                                                                                                                                                                                                PRINTS: PRO0723; SUBTILISIN.
Probom: PR00723; SUBTILISIN.
Probom: PR001717; P_domain; 1.
SWART: SW00181; EGF; 1.
PROSITE: PS00136; SUBTILASE_ASP; 1.
PROSITE: PS00137; SUBTILASE_HIS; 1.
PROSITE: PS00138; SUBTILASE_EHIS; 1.
PROSITE: PS00139; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane; Multigene family; Zymogen; Repeat.
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0A99CE8770A8E293 CRC64;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . . ) (PO

N-LINKED (GLCNAC. . ) (PO
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6; Mismatches
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(Rel. 28, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                 InterPro; IPR000561; EGF-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR00284; P_domain.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF001483; P; 1.
Pfam; PF00182; Peptidase_S8; 1.
                                                             EMBL; M94375; AAA28551.1; -.
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                                                                        PIR; A43434; A43434.
HSSP; Q99405; 1MPT.
FlyBase; FBgn0004598; Fur2
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Matches 18; Conservative
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ID TIE2_HU
AC Q02763
DT 01-FEB
DT 01-FEB
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**REQUENCE FROM N.A.

**REDINE=92381036; PubMed=1512259;

**REDINE=92381036; PubMed=1512259;

**Rentrop A., Gateff E.A.F. Leunissen J.A.M., van de Ven W.J.;

**Rentrop M., Gateff E.A.F. Leunissen J.A.M., van de Ven W.J.;

**Rentrop M., Gateff E.A.F. Leunissen J.A.M., van de Ven W.J.;

**Rentrop M., Gateff E.A.F. Leunissen J.A.M., van de Ven W.J.;

**Repression enzyme of Drosophila melanogaster with multiple RT Tepeats of a cysteine motiff.";

**J. Biol. Chem. 267:17208-17215(1992).

**C. - FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDORROFEASE CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHARYS AND CAPABLE OF ACTIVITY: Release of mature proteins from their proprocedins by cleavage of Arg-Xaa-Yaa-Arg-1-Zaa bonds, where Xaa CC an be any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                            568 DCSLGTTSCMAVNGQICNGRGVCECGA--CKCTDPKFQGPTCEMCQTCLGVCAEHKECVQ 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;

Pterygota: Nooptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                           DPLLGT -- CMSCK-TICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISCASICGQHPK--Q 62
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                    (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                29; Indels
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2)
                                                                                                                                                                                                                                                                          54340886CE157195 CRC64;
                                                                                                                 (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
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(GLCNAC...)
BY SIMILARITY.
N-LINKED (GLONG.)
                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                    Score 71.5; Di
Pred. No. 2.1;
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ΜΕ
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32.88;
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                                                                                                                                                                                                                                                                          773 AA;
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Best Local Similarity
  597
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760
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND IN PLACEMENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS MALFORMATIONS (VMCMI), AN ERROR OF VASCULAR MORPHOGENESIS CHARACTERIZED BY DILATED, SERRIGINOUS CHANNELS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                         MEDLINE=97134665; PubMed=8980225;
Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J.,
Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
                                                                                                                                                                                                                                                                                                                                                  IISSUE=Placenta;
MEDLINE=93173509; PubMed=8382358;
Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
"Molecular cloning and characterization of a novel receptor protein tyrosine kinase from human placenta.";
16-OCT-2001 (Rel. 40, Last annotation update)
Angiopoieth 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEE) (Tyrosine-protein kinase receptor TEK) (P140 TEK) (Tunica interna endothelial cell kinase).
                                                                                                                                                                                                                                                                                         "Vascular dysmorphogenesis caused by an activating mutation in the receptor tyrosine kinase TIE2.";
Cell 87:1181-1190(1996).
                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 3 FIBFONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           VARIANTS VMCM1 TRP-849 AND SER-897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000561; EGF-like.
InterPro; IPR000719; EMK_pkinase.
InterPro; IPR001961; FN III.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L06139; AAA61139.1; -.
                                                                                                                                                                                                      Oncogene 8:663-670(1993).
                                                                                                                                                                                                                                                                               Mulliken J.B., Olse B.R.
                                                                                                                                                                                                                               VARIANT VMCM1 TRP-849.
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                                                                                                                              SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=9606;
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                                                      TEK OR TIEZ.
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/FTId=VAR_006352.
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EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE DOMAIN
EGF-LIKE 1.
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PHOSPHORYLATION (AUTO
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FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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01-MAR-2002 (Rel. 41, Last annotation update)
Integrin beta-1 precursor (Fibronectin receptor
(CD29) (Integrin VLA-4 beta subunit).
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(GLCNAC.
(GLCNAC.
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N-LINKED (GLCN
N-LINKED (GLCN
N-LINKED (GLCN
                            SMART; SM00181; EGF; 2.

SMART; SM00001; EGF.11ke; 1.

SMART; SM00000; FN3; 3.

SMART; SM0219; Tyrkc; 1.

PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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EGF-LIKE 3.
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                 TYRKINASE.
pkinase; 1.
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096
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               PRINTS; PR00109;
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PCK5_HUMAN
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Expression during of a murine fibronectin receptor and its expression during inflammation. Expression of VLA-5 is increased in a retracted eperitoreal macrophages in a manner discordant from major and its deperitoreal macrophages in a manner discordant from major and its histocompatibility complex class II.";

J. Exp. Med. 169:1589-1605(1989).

C. FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-1/BETA-1 ALPHA-2/BETA-1, ALPHA-1/BETA-1, ALPHA-3/BETA-1, ALPHA-3/BETA-1, ALPHA-3/BETA-1, ALPHA-3/BETA-1, ALPHA-4/BETA-1, ALPHA-4/BETA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIDE ARRAY OF LIGANDS.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
SSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-5, ALPHA-6, ALPHA-7, ALPHA-9, ALPHA-10, ALPHA-11 OR ALPHA-V.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                   MEDLINE-89235580; PubMed-2523953;
Holers V.M., Ruff T.G., Parks D.L., McDonald J.A., Ballard L.L.,
                                                                                                                       Tominaga S.; "Murine mRNA for the beta-subunit of integrin is increased in BALB/C-3T3 cells entering the G1 phase from the G0 state."; FEBS Lett. 238:315-319(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY. SIMILARITY: CONTAINS I VWFA-LIKE DOMAIN.
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EMBL, X15202; CAA3372.1; --
PIR, PL0104; IJMSFB.
PIR, S01659; S01659.
MGD; MGI:96610; Itgbl.
InterPro: IPR000561; EGF-like.
InterPro: IPR001569; Integrin_B.
InterPro: IPR00369; Integrin_B.
InterPro: IPR003639; PSI.
InterPro: IPR002035; VWFA.
FEMM; PF00362; Integrin_B: Integrin_B.
                                                                                      STRAIN=BALB/C;
MEDLINE=89005707; Pubmed=3262537;
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ProDom; PD001811; Integrin_
                                                                                                                                                                                                               SEQUENCE OF 2-798 FROM N.A. STRAIN-BALB/C;
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                                                                     SEQUENCE FROM N.A.
                                   NCBI_TaxID=10090;
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PROSITE; PS00243; INTEGRIN_BETA; 3.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation.
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N-LINKED (GLCNAC. . .) (POTENTI
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                                                                                                                                                                               CYSTEINE-RICH TANDEM REPEATS
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                                                                                       INTEGRIN BETA-1.
EXTRACELLULAR (POTENTIAL)
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.. G us-09-854-864-16.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reudelluber T.L.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

-1 FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY
WITHIN THE CONSTITUTIVE AND REGULARED SECRETORY PATHWAY. CAPABLE
COFCLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

COFCLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

-1 CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROPROTEINS BY CLEAVAGE OF ARG. YAA. TRA. ARG. | ZAA BONDS, WHERE XAA
CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

-1 SUBCELLULAR LOCATION: Secreted (By similarity).

-1 ALTERNATIVE PRODUCTS: 2 ISOFOMNS SEEMS TO BE PRODUCED BY
ALTERNATIVE SPLICING.

-1 ALTERNATIVE SPLICING.

-1 TISSUE SPECIFICITY: EXPRESSED IN T-LYMPHOCYTES.

-1 DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
            092824; 013527;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proprotein convertase subtilisin/Kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/Kexin-like protease PC5)
(Convertase PC5) (PC6) (hPC6).
                                                                                                                                                                                                                                                                                                                                                 Miranda L., Wolf J., Pichuantes S., Duke R., Franzusoff A.; "Isolation of the human PC6 gene encoding the putative host protease for HIV-1 gpl60 processing in CD4+ T lymphocytes."; Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lu Y., Duke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Franzusoff A., Miranda L., Wolf J., Pichuantes S., Lu Y.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
  913 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lleavage on pair of basic residues; Repeat.
SIGNAL 1 32 BY SIMILARITY.
PROPEP 33 114 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
PRT;
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InterPro; IPR002884; P_domain.
InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                            TISSUE=T-cell;
MEDLINE=96353880; Pubmed=8755538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
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ProDom: PD000717; P_domain; 1.
SMART; SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U56387; AAC50643.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF 15-913 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U49114; AAA91807.1; -. HSSP; Q99405; 1MPT. MIM; 600488; -.
  STANDARD:
                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBTILASE FAMILY
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=9430371; PubMed=8069916;
Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
Rother S.C., Henzel W.J., Goeddel D.V.;
Cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
-: FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND ACTIVATES NF-KAPPA-B.
-: SUBUNIT: HOWODIMER OR HETERODIMER OF TRAFI AND TRAF2. THIS HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS FACTOR RECEPTOR 2 (TNFR2), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ------EQGKFYD 43
PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                      (BY SIMILARITY).
                                                        CYS-RICH MOTIF (CRM) REGION.
CLEAVAGE (AUTO-) (BY SIMILARITY).
CELL ATTACHMENT SITE (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                     (POTENTIAL).
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S -> F (IN REF. 3).
Y -> A (IN REF. 3).
R -> Q (IN REF. 3).
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-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
-!- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                   1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAF--C--CRK----
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                                                                                                                                                      N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
TNF receptor associated factor 2 (TRAF2).
                                                                                                                                                                                                                                                                                                                                                       Score 69; DB 1
Pred. No. 4.3;
7; Mismatches
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                              CATALYTIC.
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26.0%;
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Best Local Similarity
Matches 19; Conserv
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2225
381
665
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852
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CARBOHYD
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CHAIN
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CATALYTIC ACTIVITY: ATP + a protein tyrosine ~ ADP + protein
             tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                  (POTENTIAL)
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                        28; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                             1 CPEEQYWDPLLGTCMSCKTICNHQS----QRTCAAF-----CCRKE--QGKFYDHLLRD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 922-1097 FROM N.A.
STRAIN-SPRAGUE-PAMLEY; TISSUE-Sciatic nerve;
MEDLINE-97184212; PubMed-9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and ExbB3, is Induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ERB3_RAT G2955; PRT; 1339 AA. G2955; G2955; G2955; G2958; G296799 (Rel. 37, Created) 15-DEC-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) ERBB-3 receptor protein-tyrosine kinase precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY, TISSUE-Liver;
MEDLINE-96096535; PubMed-8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;
"Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
Gene 165:279-284(1995).
                                                                                                                                                                                                                                                                                    DB 1; Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  043B391180365F10 CRC64;
                                                                                                                                                                                                                   TRAF-TYPE 2. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                  16.9%; Score 68.5; Di
ilarity 25.0%; Pred. No. 3;
Conservative 10; Mismatches
                                                                                                                                                                                              RING-TYPE.
TRAF-TYPE 1.
           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                         MATH/TRAF
                                                                                                                                                                                     Coiled coil; Repeat.
                            EMBL, L35303, AAC37662.1, -.
MGD; MGI:101835; Traf2.
InterPro; IPR002083; MATH.
InterPro; IPR0013007; TRAF.
InterPro; IPR0011841; Znf-TRAF.
Pfam; PF00917; MATH; 1.
Pfam; PF0097; Zf-C3HC4; 1.
SMART; SM00061; MATH; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                  PROSITE; PSO0518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50145; ZF_TRAF; 2.
                                                                                                                                                                                                                                                    56026 MW;
                                                                                                                                                                                                                                                                                                                                                                                     209 CSKCRVLCRFHTVGCS 224
                                                                                                                                                                                                                                                                                                                                                                      49 CISCASICGOHPKQCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                  501 AA;
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                                                                                                                                     Zinc-finger;
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Best Local S
Matches 19
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SEQUENCE
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ZN_FING
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DOMAIN
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Interpro: IPR000419; Euk_pkinase.

Interpro: IPR000719; Euk_pkinase.

Interpro: IPR000719; Euk_pkinase.

Interpro: IPR001245; Tyr_pkinase.

Interpro: IPR001245; Tyr_pkinase.

Interpro: IPR001245; Tyr_pkinase.

Interpro: IPR001245; Tyr_pkinase.

Interpro: IPR00134; Interpro: II.

Interpro: IPR00134; Interpro: II.

Interpro: IPR00136; INTERINASE.

INTERPRO: IPRO: IP
SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTW. LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES PHOSPHATIDYLINOSITOL 3-KINASE.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERBB-3 RECEPTOR PROTEIN-TYROSINE KINASE. EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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F120281D432423D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                   EUL. J. BIOCHEM. 177:35-45(1988).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-!- SUBUNIT: LAMININ IS A COMFLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPRIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                               MEDLINE-89030693; PubMed-3181157; Deutramen I., Hartl L.; Deutramen R., Huber J., Schmetz K.A., Oberbaeumer I., Hartl L.; Structural study of long arm fragments of laminin. Evidence for repetitive C-terminal sequences in the A-chain, not present in the B-chains.";
                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89034134; Pubmed=3182802;
Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;
"Laminin, a multidomain protein. The A chain has a unique globular domain and homology with the basement membrane proteoglycan and the
                                                                                                                                                                                                                                                                         SEQUENCE OF 1-339 FROM N.A.
MEDILINE-88225080; PubMed=3267223;
Hartl L., Oberbaeumer I., Deutzmann R.;
"The N terminus of laminin A chain is homologous to the B chains.";
Eur. J. Blochem. 173:629-635(1988).
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMININ-3 (S-LAMININ).
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Laminin alpha-1 chain precursor (Laminin A chain).
LAMA1 OR LAMA-1 OR LAMA.
Mus musculus (Mouse).
                                   PRT; 3084 AA.
                                                                                                                                                                                                                                                   Biol. Chem. 263:16536-16544(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A31771; MAMASA.
HSSP; P02468; 1TLE.
MGD; MGI:99892; Lamal.
InterPro; IPR000561; EGF-like.
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EMBL; X13459; CAA31807.1; -.
EMBL; M36775; AAA39406.1; -.
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LMA1_MOUSE
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STRAIN-B6/C3; TISSUE-Liver;
STRAIN-B6/C3; TISSUE-Liver;
MEDLINE-94170986; PubMed-8125255;
MEDLINE-94170986; PubMed-8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
"The mouse waved-2 phenotype results from a point mutation in the EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
SUBCELULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.; "Comparison of EGF receptor sequences as a guide to study the ligand
                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                Avivi A., Skorecki K., Yayon A., Givol D.; "Promoter region of the murine fibroblast growth factor receptor
               Epidermal growth factor receptor precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                     Hibbs M.L.; Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                SEQUENCE FROM N.A. CRANDER STARAN-BALLACK, AND CD-1; TISSUB-Liver, and Decidua; MEDLINE-93126580; pubmed-7678348; Paria B.C., Das S.K., Andrews G.K., Dey S.K.; Paria B.C. bas barkersasion of the epidermal growth factor receptor in moural barkersts during delayed implantation."; Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
  15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                       STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-93026370; Pubmed-1408137;
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MEDLINE-91232866; Pubmed-2030916;
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STRAIN-BALB/C; TISSUE-Liver;
                                                                                                                                                                           (bek/KGFR) gene.";
Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor tyrosine kinase.";
Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-714 FROM N.A.
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EMBL; X78987; CAA55587.1; -. EMBL; U03425; AAA17899.1; -. EMBL; X59698; CAA42219.1; -.

(Rel. 33, Created) (Rel. 33, Last sequence update)

01-FEB-1996 01-FEB-1996 EGFR_MOUSE Q01279;

PRT; 1210 AA

STANDARD;

EGFR_MOUSE RESULT

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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) MAJOR SITE)
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
TYCOSine-protein Kinase; ATP-binding; Phosphorylation; Repeat.
SIGNAL 1 24 POTEMIAL.
                                                                                                                                                                                                                                                                                                          POTENTIAL.
EPIDERMAL GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 1; Length 1210;
Pred. No. 8.7;
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690E20D46DF2D2F5 CRC64;
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PHOSPHORYLATION (BY PKC)
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N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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CYTOPLASMIC (POTENTIAL).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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C -> W (IN REF. 5)
L -> F (IN REF. 4)
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01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
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                                            MGD; MGI:95294; Egfr.
InterPro; IPR000494; EGFR_L,
InterPro; IPR000119; Euk_phinase.
InterPro; IPR00174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
Ffam; PF00757; Furin-like; I.
Ffam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain; 2.
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175 175 N-LI
196 196 196 N-LI
352 352 N-LI
413 413 N-LI
544 444 N-LI
568 568 N-LI
603 603 N-LI
613 623 N-LI
19 19 C C ->
99 99 99 C C ->
1116 1117 HP -
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565 QAMNITCTGRGPDNCIQCAHY 585
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EMBL; L06864; AAA53029.1; -. EMBL; Z12608; CAA78249.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.5%;
Best Local Similarity 27.2%;
Matches 22; Conservative
                                                                                                                                                                                SMART; SM00261; FU; 3.
SMART; SM00219; TYFKC; 1
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PARACKET S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,

Marzluf G.A., Amato A.A., Mendell J.R.;

Hum. Mutat. 13:340-340(1999).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ

-!- STHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF

CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING

MITH OTHER EXTRACELLULAR MATHIX COMPONENTS.

-!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE

DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND

TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE

COMPRISING ONE LONG & THREE SHORT ARMS WITH GLABULES AT EACH END.

THE ALPHA-Z. CHAIN IS A SUBUNIT OF LAMININ-2 (MÉROSIN) AND LAMININ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRARES (WAJOR COMPONENT).

-1 TISSUE SPECIFICITY: PLACENTA, STRIATED MUSCLE, PERIPHERAL NERVE, CARDIAC MUSCLE, PANCREAS, LUNG, SPLEEN, KIDNEY ADRENAL GLAND, SKIN, TESTIS, MENINGES, CHOROID PLEXUS, AND SOME OTHER REGIONS OF THE BRAIN; NOT IN LIVER, THYMUS AND BONE.

-1 DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COLLED COLL STRUCTURE.

-1 DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.

-1 DISEASE: DEFECTS IN LAWAZ ARE THE CAUSE OF MEROSIN-DEFICIENT CONGENITAL MUSCULAR DYSTROPHY (MCMD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
Hirvonen H., Shows T.B., Sariola H., Engvall E., Thygyason K.;
"Human laminin M chain (merosin): complete primary structure,
chromosomal assignment, and expression of the M and A chain in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97066955; PubMed-8910357;
MEDLINE-97066955; Volteen P., Tryggvason K.;
Structure of the human laminin alpha2-chain gene (LAMA2), which is affected in congenital muscular dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LRS-2614.
Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
Marzluf G.A., Amato A.A., Mendell J.R.;
Novel single base polymorphisms and rare sequence variants in
the laminin 2-chain coding region detected by RNA/SSCP analysis.";
Hum. Mutat. 13:174-174(1999).
                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
-!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (S-MEROSIN).
SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E., "Mercosin, a Lissue-specific basement membrane protein, is a laminin-like protein,", Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
                                                                              LAMAZ OR LAMM.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
Laminin alpha-2 chain precursor (Laminin M chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 271:27664-27669(1996).
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MEDLINE=90238994; PubMed=2185464;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=94124633; PubMed=8294519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Biol. 124:381-394(1994).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMININ ALPHA-2 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 15.
LAMININ EGF-LIKE 16.
LAMININ EGF-LIKE 16.
LAMININ EGF-LIKE 16.
LAMININ EGF-LIKE 17.
LAMININ G-LIKE 17.
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01-JUL-1993 (Rel. 26, Last sequence update)
01-MR-2002 (Rel. 4) Last annotation update)
17 umor necrosis factor receptor superfamily member 17 (B-cell
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Pred. No. 18;
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30.5%;
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TNFRSF17 OR BCMA OR BCM.
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      InterPro; IPR001886;
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TR17_HUMAN
TD TR17_HUMAN
AC 00223;
DT 01-JUL-1993
DT 01-JUL-1993
DT 01-MAC-2002
DE TUMOR NECROS
DE MALITATION P
GN TNFRSF17 OR
OS HOMO SAPIENS
OC EUKARYOLA; M
OC MARMADIA; EU
OX NCBI_NASID-9
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                 AAB18388.1; JAB1818388.1; JAB18388.1; JAB18388.1; JAB18388.1; JAB18388.1; JAB18388.1; JAB18388.1; J
                                                                                                             EMBL; Z26653; CAA81394.1;
EMBL; U66796; AAB18388.1;
EMBL; U66733; AAB18388.1;
EMBL; U66734; AAB18388.1;
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99425270; PubMed=10493829;
MEDLINE-99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
             SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
TISSGE-PETIPHERAL Blood leukocytes, and Lymph node;
MEDLINE=93010984; PubMed=1396583;
Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
Larsen C.J., Tsapis A.;
Tanjis A.;
A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
EMBO J. 11:3897-3904(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20259066; PubMed-10801128; Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R., Gross J.A., Johnston J., Mudri S., Enselman R., Lofton-Day C., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Harrison K., Kindsvogel W., Clegg C.H.; "TACI and BOMA are receptors for a TNF homologue implicated in B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF.
-1- TISSUE SPECIFICITY: EXPRESSED IN MATURE B-CELLS.
-1- DISBAGE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13) WHICH INVOLVES BCMA AND IL2.
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"TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-activated protein kinase.";
J. Immunol. 165:1322-1330(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.; "New polymorphisms of human BCMA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             Laabi Y., Gras M., Brouet J., Berger R., Larsen C., Tsapis A.;
"The BCMA gene, preferentially expressed during B lymphoid
maturation, is bidirectionally transcribed.";
Nucleic Acids Res. 22:1147-1154(1994).
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                                                                                                                                                                                                                                          MEDLINE=94218235; PubMed=8165126;
Laabi Y., Gras M., Brouet J., Ber
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Nature 404:995-999(2000).
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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EMBL; U95742; AAB67251.1; -. EMBL; AB052772; BAB60895.1;

229575; EMBL; Z29574;

EMBL;

EMBL, ABO52772; BAB60895.1; PIR, S31208; S31208. PIR, S31209; S31209. MIM; 109545;

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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.

1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-11/BETA-1 AND ALPHA-2/BETA-1, ALPHA-2/BETA-1, ALPHA-2/BETA-1, ALPHA-4-BYBETA-1, ALPHA-4-BYBETA-1, ALPHA-4-BYBETA-1, ALPHA-4-BYBETA-1, ALPHA-4-BYBETA-1, ALPHA-11/BETA-1 AND ALPHA-1/BETA-1 AND ALPHA-1/BETA-1, ALPHA-1/BETA-1 AND ALPHA-1/BETA-1 IS A RECEPTOR FOR FIBRINGENIN ALPHA-1/BETA-1 IS A RECEPTOR FOR FIBRINGENIN ALPHA-1/BETA-1 AND ALPHA-2/BETA-1, ALPHA-2/BETA-1 AND ALPHA-1/BETA-1 AND ALPHA-1/BETA
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                                                                                                                                                                                                                                                                                                            1;
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Receptor; Proto-oncogene; Transmembrane; Chromosomal translocation;
                                                                   BREAKPOINT FOR TRANSLACATION TO FORM INTERLEUKIN 2/BCM ONCAGENE.
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Felis.
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01-0cT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1ntegrin beta-1 precursor (Fibronectin receptor beta subunit)
(CD29) (Integrin VLA-4 beta subunit).
                                                                                                                                                                                                                                                        Length 184;
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277AF11E2767D932 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae
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(G. ) (POTENTIAL)
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PROSITE; PS00022; EGF_1; UNKNOWN_2.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation.
SIGNL 21 798 INTEGRIN BETA-1.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
VWFA-LIKE.

4 CYSTEINE-RICH TANDEM REPEATS.
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III.
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InterPro; IPR002369; Integrin_B.
InterPro; IPR00169; Integrin_beta_C.
InterPro; IPR00169; PSI.
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InterPro; IPR002035; VWFA.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	O14836 homo sapien O9dbz3 mus musculu		095980 homo sapien	Q26489 spodoptera	007571 bacillus su	Q26033 plasmodium	P92163 strongyloce	Q9hav5 homo sapien	074567 trichoderma	Q9bps2 bombyx mori	Q9d2h5 mus_musculu	Q991e4 mus musculu	035171 mus musculu	Q62030 mus musculu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CPKDQYWDSSRKSCVSCALTCSQRSQRTCTDFCKFINCRKEQGRYYDHLLGACVSCDSTC 65
                                                                                                                                                                                                                          Eukaryota; Metzezoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%; Score 256; DB 11; Length 249; 57.7%; Pred. No. 3.9e-26; ative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, ancoroco, and Mar. MGD; MGI:1889411; Infrsf13b. GF4290D719FEA037 CRC64; GF01BNCE 249 AA; 26981 MW; 6F4290D719FEA037 CRC64;
                                                                                                                            Last sequence update)
Last annotation update)
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Last sequence update)
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                                                 249 AA
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                                                                                                  Created)
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=LUNG;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mature 409:685-690(2001).
EMBL; AK004668; BAB23457.1; -.
                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                   1200009E08RIK PROTEIN.
TNFRSF13B OR 1200009E08RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111:111:11
TQHPQQCAHFC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 GQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACI PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ET35;
                                                                           Q9DBZ3
                                                 09DBZ3
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RESULT
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                          1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC----CRKEQGKFYDHLLRDCISCASIC 56
                                                                                                                                                                                                                                                                                6 CPKDQYWDSSRKSCVSCALTCSQRSQRTCTDFCKFINCRKEQGRYYDHLLGACVSCDSTC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LGTC----MSCKTICNHQSQRTCAAFCCRKE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hitomi K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y., Ratxkin B.J., Arakawa T., Noda M.; Regulation of matrix metalloproteinase-9 and inhibition of tumor invasion by the membrane-anchored glycoprotein RECK."; Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86.5; DB 11; Length 971;
Pred. No. 0.0046;
8; Mismatches 28; Indels 35
                                                                                                                                                                  63.2%; Score 256; DB 11; Length 249; 57.7%; Pred. No. 3.9e-26; 1.ve 11; Mismatches 15; Indels
971 AA; 106134 MW; 2FC8EBE38A20F86D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 QGKFYDHLLRDCIS-----CASICGQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               971 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   971 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00282; KAZAL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99007295; PubMed-9789069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%;
26.8%;
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(TrEMBLrel. 10, 1)
(TrEMBLrel. 19, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1855698; Reck.
InterPro; IPR002350; kazal.
Pfam; PF00050; kazal; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPEE--QYWDPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.89
Matches 26; Conservative
                                                                                                                                                                                            Best Local Similarity 57.7
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                       66 ТОНРООСАНЕС 76
                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                                                               57 GQHPKQCAYFC
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                                                                                                                                                                                                 MEDITINE—9000, Takabashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K., Ritaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y., Ratzkin B.J., Arakawa T., Noda M.; "Regulation of matrix metalloproteinase-9 and inhibition of tumor invasion by the membrane-anchored glycoprotein RECK."; EMBL; D50406; BAA34060.1; A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID=7108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-SEP, FALL MANYWORM OVARY; Cieplik M., Kahi AMYWORM OVARY; "Cloning and functional characterization of FURIN from Spodoptera
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.9%; Score 84.5; DB 4; Length 971; 25.8%; Pred. No. 0.0085; ive 10; Mismatches 27; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frugiperda (Sf9) cells.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 26888; CAA93116.1; -.
HSSP: Q99405; IMPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL 1 20 FULENITAL.
SEQUENCE 971 AA; 106457 MW; 173047D6AEE6F834 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ----YENALFSCISRNEMGSVCCSTAGHH-TNCREYC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 QGKFYDHLLRDCIS-----CASICGQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR002174; Furin-like.
InterPro: IPR00209; Peptidase_S8.
InterPro: IPR002884; P_domain.
Pfam; PF001483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF000723; SUBTILISIN.
ProDom; PD000712; P_domain; 1.
SMART; SM00261; FU; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00282; KAZAL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002350; kazal.
SMART; SM00280; KAZAL; 3.
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Best Local Similarity 25.87
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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01-DEC-2001 (TrEMBLrel.
ENDOPROTEASE FURIN.
ST15 PROTEIN PRECURSOR.
                                                      Homo sapiens (Human)
                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                    NCBI_TaxID=9606;
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Q26489
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A Kunst F., Ogasawara N., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barasher L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Entiac S., Erington J., Fabret C., Ferrari E., Foulger D., Faritz C., Fujita M., Fujita Y., Fumer S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Hagad K., Halech J., Harwood C.R., Henaut A., R. Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Andiseppi G., Guy B.J., Hagad K., Halech J., Harwood C.R., Henaut A., R. Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Andia W., Kollas B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Karahara Y., Koningstein G., Krogh S., Kunback M., Redigue C., Media W., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C., Media W., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C., Media W., Mellado R.P., Mixuno M., Moestl D., Porwollik S., Prescent E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Resecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Sato T., Scanlan E., Schleich S., Schroeber, Rose M., Sacot I., Takamakoshi A., Tarakashi H., Taramakoshi A., Tarakashi H., Taramakoshi A., Taramakoshi A., Tarakashi H., Taramakoshi A., Taramakoshi A., Taramakoshi A., Taramakoshi A., Taramanoto H., Wannane K., Yasamotti A., Wannancter P., Wanbutt R., Wadheler E., Waldler E., Waldler H., Wannanck C., Taramakoshi A., Taramanoto H., Yamamoto H., Yamamoto K., Yasamotti A., Wanbutt R., Wadhutt R., Wadheler E., Waldler E., Waldler E., Waldler E., Waldler H., Wannanck C., Wan
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                    1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAA----FCCRKEQGKHYDHLLRDCISCASIC 56
                                                                                                                                                                                         13;
                                                                                                          ength 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bron S.;
                                                                                                                                                                                         Indels
1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04, Created)
04, Last sequence update)
08, Last annotation update
                                                                                                                      Score o...,
Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                  DB 5;
                                                                                                                                                                                         5; Mismatches
                                                                                                                  Score 81.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLRE1 04, Cr. 01-JUL-1997 (TREMBLRE1 04, La. 01-VUY-1998 (TREMBLRE 08, La. HYPOTHETICAL 11.8 KDA PROTEIN.
                                                                                                              20.1%;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 GVTNSTPPTDCCH 1183
                                                                                                                                                                                                                                                                                                                                                                                                                  57 G----QHPKQCAY 65
                                                                                                                                                      Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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   SEQUENCE
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                                                                                                                  Query Match
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Integrin; Repeat; T
SEQUENCE 783 AA;
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SEQUENCE
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Q9HAV5
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                       EQYWDPLLGTCMSCKTICNH------33
                                                                                                                                                             2 EQYSEACIEACIDCMKACNHCFTKCLEESVQHHLSGCIRLDRECADICALAVKAMQTDSP 61
                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-55330813; PubMed-7606788; Su X.Z., Heatwole V.M., Werthelmer S.P., Guinet F., Herrfeldt J.A., Su X.Z., Heatwole V.M., Werthelmer S.P., Guinet F., Herrfeldt J.A., Peterson D.S., Ravetch J.A., Wellems T.E., "The large diverse gene family var encodes proteins involved in cytoadherence and antigenic variation of Plasmodium falciparum-fafected erythrocytes."; Cell 82:89-100(1995).

EMBL; L40609; AAA75398.1; -.

InterPro; IPRO04258, PFEMP.
                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                           Score 80; DB 16; Length 108;
Pred. No. 0.004;
7; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 5; Length 2664;
Pred. No. 0.23;
4; Mismatches 9; Indels
Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: Y14081; CAA744791; -.
EMBL: 299109; CAB12900.1; -.
Hypcthetical protein; Complete proteome.
SEQUENCE 108 AA; 11839 MW; 78637689ABB0FD8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )11; PFEMP; 2.
2664 AA; 302410 MW; 6EA2468511703091 CRC64;
                                                                                                                                                                                                FMKEICALCADICEACGTECGKHDHDH----CQACAKACFTCAEGC 103
                                                                                                                                                                                   34 ------CRKEQGKF-YDHLLRDCISCASICGQHPKQC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VARIANY-SPECIFIC SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 FCCRKEQGKFYDHLLRDCISCAS----ICGQHPKQC 63
                                                                                                                                                                                                                                                                 PRT; 2664 AA
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                                                                                           19.8%; 22.6%;
                                                                                                                24; Conservative
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                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-FCR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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P92163;
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                                                                                                                 Matches
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Q26033
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Gaps
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Marsden M., Burke R.D.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-2045245; bubMed=11039935;
Wan M., Wang L.C., Hymowitz S.G., Schilbach S., Lee J., Goddard A., de Vos A.M., Gao W.O., Dixit V.M.;
"Two-mains acid molecular switch in an epithelial morphogen that regulates binding to two distinct receptors.";
Science 290:523-527(2000).
EMBL, AF298812; AAC38761.1; -.
InterPro; IPR001368; TMFR_C6.
Pfam; PF00020; TWFR_C6; 2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS0002; EGF_1; UNKNOWN_2.
PROSITE; PS0186; EGF_2; UNKNOWN_1.
PROSITE; PS010243; INTEGRIL BETA; 2.
Cell adhesion; Gytoskeleton; Extracellular matrix; Glycoprotein; Integrin; Repeat; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
S
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                                                                                                                 BONDS (BY STILLARITY).

--- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.

BENBL, 077584; AAB39739.1; --

REMBL, 077587; AAB39739.1; --

RICEPTO: IPRO00561; EGF-11ke.

RICEPTO: IPRO0169; Integrin_B.

RICEPTO: IPRO0169; Integrin_beta_C.

RICEPTO: IPRO0269; PSI.

RICEPTO: IPRO0269; PSI.

RICEPTO: IPRO0269; PSI.

RICEPTO: IPRO0169; Integrin_beta_C.

RICEPTO: IPRO0169; Integrin_beta_C.

RICEPTO: IPRO0169; Integrin_B: 1.

RECODOM: PD00181; Integrin_B: 1.

RECODOM: PD00187; INDE; 1.

SMART; SM000187; INB: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB045C6F6D88FBB2 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
x-LINKED ECTODYSPLASIN-A2 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.9%; Score 76.5; DB
33.3%; Pred. No. 0.08;
tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 33.39
Matches 19; Conservative
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SMART; SM00327; VWA; 1
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3;

12; Gaps

28;

723 AA.

Length 1069; Indels

DB 5;

us-09-854-864-16.rspt

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Carraine Control N. T. Subsections of the March 
                                                                                                                                                                                                                                                                                                                                                                                                        257 CADNYYGDPLRGTCEKCE--CNENIDITKPGNC-----DPYFGKCLQCLYNTAGEH 305
                                                                                                                                                                                                                                                                                                                                                                        1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISCA-SICGQH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                            DF40F37A0CCA79A4 CRC64;
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"Functional annotation of a full-length mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
       SMART; SM00180; EGF_Lam; 8.

SMART; SM0001; EGF_Like; 1.

PROSITE; PS00022; EGF_1; UNKNOWN_6.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_8.

EGF-like domain; Glycoprotein.

1 1

SEQUENCE 1069 AA; 118894 WW; DF40F37AOCCA7;
                                                                                                                                                                                                                                                                                              Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                      Score 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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EMBL; AK019654; BAB31824.1; -.
MGD; MGI:1926161; 4930486B16Rik.
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InterPro; IPR000315; Znf_bbox.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                      18.5%;
29.7%;
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Pfam; PF00643; zf-B_box; 2.
                                                                                                                                                                                                                                                                 Query Match 18.55
Best Local Similarity 29.77
Matches 19; Conservative
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SMART; SM00060; FN3; 1.
SMART; SM00184; RING; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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EMBL, X55671, ZA646974.1; -...
Interpro: IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 CPDSQYWD---GSKCACPYGTVWDCKHCNQDCGKDAHFDSNQKKCV---CNK-QGEVYDS 561
*3 CQENEYWDQ-WGRCVTCQR-CGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPEEQYWDPLLGTCMSCK--TI-----CNH-----QSQRTCAAFCCRKEQGKFYDH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBI_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 18.6%; Score 75.5; DB 3; Length 704; Local Similarity 28.6%; Pred. No. 0.098; es 28; Conservative 9; Mismatches 20; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kang W., Zemskov E.A., Imai N., Iwanaga M., Suzuki M.G.;
"Characterization of interaction between Bombyx mori
nucleopolyhadrovirus BRO-A and host LAMININ-like protein.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB046365; BAB21565.1; -.
HSSP; P02468; ITLE.
InterPro; IPR000561; EGF-like.
InterPro; IPR000549; Laminin_EGF.
Pfam; PF00053; laminin_EGF: 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Glycoprotein.
704 AA; 77925 MW; 63414BDDEC365EBC CRC64;
                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CECT 2413;
MEDLINE=98263335; PubMed=9600944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bombycoidea; Bombycidae; Bombyx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                           08,
08,
19,
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                                                                                                                                                                                                                                                                 074567;
01-NOV-1998 (TrEMBLrel. 01
01-NOV-1998 (TrEMBLrel. 01
01-DEC-2001 (TrEMBLrel. 1)
Q174 PROTEIN.
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                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Trichoderma harzianum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMININ (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                            49 CISCASI 55
                                                                                                               CITCAVI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
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01-DEC-2001
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Best Local Si
Matches 28;
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                                                                                                                                                                                      RESULT 11
074567
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Q9BPS2

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EMBL; AF008222; AAB95315.1; -.
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STRAIN-BALB/C;
MEDLINE-980653888; PubMed-9393739;
MEDLINE-980653888; PubMed-9393739;
Mai#s R.E., Goodrow T.L., Liu S.C., Brilliant M.H., Basset P.,
Mai#s R.E., Klein-Szanto A.J.;
"Expression of PACE4 in chemically induced carcinomas is associated
with spinole cell tumor conversion and increased invasive ability.";
Cancer Res. 57:5226-5231(1997).
                                                                                                                                                   9 PLLGTCMSCKTICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFC 67
                                                                                                                                                                                        19 PRLFSCLCCKFI--FTSERNCTCFPC----PYKDE--RNCQFCHCTCAENP-NCHWCC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PCSK6 OR PACE4.

Mus musculus (Mouse),

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthela; Rodentia; Sciurognathi; Muridae; Musines; Musin
                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 CMSCKT-ICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISC---ASICGQHPKQC
                                             18.3%; Score 74; DB 11; Length 723; 32.2%; Pred. No. 0.16; artive 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC003302; AAH03302.1; -- MEROPS; SOB.075; --
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213 AA; 23781 MW; 39AlD5235454ECB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO SUBTILISIN-LIKE ENDOPROTEASE (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000345; CytC, heme_bind.
InterPro: IPR000345; CytC, heme_bind.
InterPro: IPR000561; EGF-like.
InterPro: IPR0003174; Furin-like.
InterPro: IPR000322; Znf-C2H2.
SMART; SM00181; EGF; 3.
SMART; SM00261; FU; 4.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                        213 AA
                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                   19; Conservative
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                                          Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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01-JUN-2001
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SEQUENCE
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Q99LE4
                                                                                                      Matches
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Matches
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                                                                                                                                                                                                                                                           17.7%; Score 71.5; DB 11; Length 296; 29.6%; Pred. No. 0.14; tive 7; Mismatches 24; Indels 7;
                                                                                                                                                                               MEROPS; SOB.075; -..
MEROPS; SOB.075; -..
MGD: MGI:102897; Pcsk6.
InterPro; IPR000561; Furin-11ke.
InterPro; IPR000822; Znf-C2H2.
SMART; SM000181; EGF; 2.
SMART; SM00001; EGF_11ke; 1.
SMART; SM00001; EGF_11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 25, 2002, 16:24:31
Job time: 661 sec
                                                                                                                                                                                                                                                           Query Match 17.7
Best Local Similarity 29.6
Matches 16; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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67 405 1 CPEEQYWDPLLGTCMSCKTI.....DCISCASICGQHPKQCAYFC US-09-854-864-16 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

747574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_032802:* • • Database

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989_DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980_DAT:*
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/SIDSI/gcgdata/geneseqg-embl/AA1987. DAT:*
/SIDSI/gcgdata/geneseqg-embseqgeneseqg-embl/AA1988. DAT:* 14: 15: 17: 17: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human lymphocyte s	Human TACI splice	Human lymphocyte s	Human neutrokine-a	A transmembrane ac	Human TACI protein	Human tumour necro	A murine ztnf4, a	Human BR43x2, an i	Human secreted pro	Homo sapiens vascu
SUMMARIES	ID	AAW75785	NAE09244	AAW75783	AAB36312	AAY94000	AAE09240	AAY71914	AAY94006	AAY93998	AAB65001	AAW53240
		19	22	19	21	21	22	22	21	21	22	19
	Match Length DB	166	265	293	293	293	293	293	249	247	220	325
*	Match	97.0	97.0	97.0	97.0	97.0	97.0	97.0	63.2	50.4	20.9	18.9
	Score	393	393	393	393	393	393	393	256	204	84.5	76.5
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(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL. 97US-0810572. 98WO-US04270

3-MAR-1998; 03-MAR-1997;

Homo sapiens WO9839361-A1 11-SEP-1998. Bram RJ, Von Bulow G; WPI; 1998-506346/43. N-PSDB; AAV57330.

Human VEGF-D prote Human zvegf2 growt Homo sapiens vascu Human vascular end Human VEGFD protein Human VEGFD protein Human prepro-vascu Human vascular end	Human Vascular end Human Vascular end Human Vascroll prot Human C-Fos induce Human C-Fos induce Human TANGO 140-2. Human TANGO 140-2. Human TANGO 140-1. Human TANGO 140-1. Human uterine myom Human uterine myom Human uterine myom Human uterine myom Human TANGO 180-100-100-100-100-100-100-100-100-100-	Drosophila melanog Drosophila melanog Human novel KIAA12 Human novel KIAA12 Novel human protei	domain. r; man; mphocyte; une disease; sus host disease;
AAY97572 AAW49036 AAW53241 AAW1293 AAB10649 AAR29049 AAY70750	AAN 00441 AAB 70685 AAB 37606 AAW 14994 AAW 1318 AAW 03118 AAB 01421 AAB 01421 AAB 01421 AAB 29534 AAB 29534 AAB 33477 AAW 03116 AAB 29533 AAR 41662 AB 841017	ABBG0503 AAB10608 AAE10610 AAE07870 ALIGNMENTS	extracellular CAML-interactc Lin ligand; hu ;; B-cell; B ly ritis; autoim ive; graft ver inal transducti
221 221 221 221 221 231	222222222222222222222222222222222222222		try) ce recept trivator e ting cycle eptor; hu umatoid e munosuppx therapy;
88888888888888888888888888888888888888	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 A A A A A	st entry) surface r ne activa dulating theunating receptor receptor receptor receptor receptor receptor receptor receptor receptor
		7. 7. 7. 7. 7. 7. da	95; -1999 (first lymphocyte sur transmembrane m signal-modul cyte surface r dion; cancer; r ulonephritis;
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	2007 2007 2007 2007 2007 2007 2007 2007	71.5 71 71 71 71 71 75785	AAM75785; 18-JAN-1999 (first entry) Human lymphocyte surface receptor TACI; transmembrane activator and calcium signal-modulating cyclophi lymphocyte surface receptor; human infection; cancer; rheumatoid arth glomerulonephritis; immunosuppress transplant rejection; therapy; si
112 113 114 118 118	24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	SUL W75	X X X X X X X X X X X X X X X X X X X

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                                                                            This is the amino acid sequence of the N-terminal, i.e. the extracellular, domain of novel human transmembrane activator and caxtracellular, domain of novel human transmembrane activator and caxtracellular, domain of novel human transmembrane activator and caxtracellular is involved in Taxti sa lymphocyte receptor protein that is involved in a much lesser extent it is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. The extracellular domain of Taxi functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the C-terminal portion (see Amy7784) of Taxi to the N-terminal domain of CAMI. A recombinant form of the caxtracellular portion of TAXI acts as a dominant-negative or blocking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or careful versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TAXI, in which cativation of the AP-1, CAMP or NF-KB pathway, of NF-AT cranscription.
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                                                                                                                                                                                                                                                                                                                                                                                                             1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC----CRKEQGKFYDHLLRDCISCASIC 56
                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                Length 166;
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                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Pred. No. 6.4e-33;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ, Dodge KH, Grewal I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE09244 standard; Protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TACI splice variant protein.
                                                        Claim 8; Page 73; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                94.08;
                                                                                                                                                                                                                                                                                                                                                                          94.48;
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2000US-0226986
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                                                                                                                                                                                                                                                                                                                                                                                      67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 GQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                           Sequence 166 AA;
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New isolated
products for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09244;
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                    disease
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4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BGMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psorlasis and lupus erythematosus. The present sequence is human
                                                          Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACI; transmembrane activator and CAML-interactor; calcium signal-modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B-cell; B lymphocyte; infection; cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis; lamunosuppressive; graft versus host disease; transplant rejection; therapy.
                                                                                                                                                                                                                                                                            The invention relates to methods of using one or more agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 393; DB 22; Length 265;
Pred. No. 9.9e-33;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Extracellular_domain
/note= "Claim 8"
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/note- "Claim 6"
34..71
/note- "TNFR_NGFR motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lymphocyte surface receptor TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW75783 standard; Protein; 293 AA.
                                                                                                                                                                                                                     Example 1; Fig 6; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACI splice variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 GQHPKQCAYFC 67
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9839361-A1
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                                                                                                                                                              antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                     cativator and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TACI is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. TACI cDNA (seev57328) was isolated from a B-lymphocyte convaling a yeast two-hybrid assay. Also claimed are activity. TACI cDNA (seev57328) was isolated from a B-lymphocyte convaling a yeast two-hybrid assay. Also claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments of TACI, recombinant DNA constructs, unicellular hosts, and antibodies to TACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes without affecting injand for TACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes immune system activity, e.g. for treating infections or cancers. It can be blocked to provide immunosuppression, e.g. for treating infections and inflammatory conditions such as immune complexing mysthenia gravis, type II collagen-induced arthritis, experimental mysthemia gravis, type II collagen-induced arthritis, experimental systemic lupus erythematosus, transplant rejection, cancer or system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant; ophthalmological; gene therapy; immunodeficiency disorder; diagnosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neutrokine-alpha binding protein; NAR protein; TR17; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC----CRKEQGKFYDHLLRDCISCASIC 56
                                                                                                                                                                             products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host
                                                                                                                                                               New isolated transmembrane activator protein - used to develop
                                                                                                                                                                                                                                                            This is the amino acid sequence of novel human transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 393; DB 19; Length 293;
Pred. No. 1.1e-32;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neutrokine-alpha binding protein TR17 SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                 (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36312 standard; Protein; 293 AA.
                                                                                                                                                                                                                                  Claim 20; Fig 2a; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.0%;
                                        97US-0810572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Conservative
                                                                                             Von Bulow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-506346/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AA;
                                                                                                                                     N-PSDB; AAV57328
              03-MAR-1998;
                                        03-MAR-1997;
                                                                                                                                                                              products for
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                                                                                             Bram RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                          disease
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Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; strif4 activity; antibody production; autoimmune digease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; nephritis; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the human neutrokine-alpha binding (NAR) protein designated TR17. TR17 has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiallergit, hepatotropic, antidiabetic, antiinflammatory, antiulcer, cardiant and ophthalmological activities and can be used in gene therapy. The TR17 protein and antibodies are useful for treating and diagnosing immunodeflociency polynucleotides, antibodies, agonists and/or antagonists are used for treating various other diseases defined in the specification and as research tools for studying the phenotypic effects that result from inhibiting TR17/TR17 ligand interactions on various cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding a neutrokine-alpha receptor (NAR) such as TR17, useful for producing TR17 protein which is used in the treatment and diagnosis of autoimmune and immunodeficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 393; _____
Pred. No. 1.1e-32; _____
---+_hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 398pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                 24-MAR-2000; 2000WO-US07966.
                                                                                                                                                                                                                                                                                                        10-MAR-2000; 2000US-0188208
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Matches 67; Conservative
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                                                          WO200058362-A1
Homo sapiens.
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                                                                                                                               05-OCT-2000
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Homo sapiens

13-JUL-2000

07-JAN-1999;

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Marsters SA, Pitti RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL block the interaction between APRIL and APRIL APRIL APRIL APRIL AND APRIL AND APRIL AND APRIL AND APRIL AND APRIL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour necrosis factor receptor (TACI) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.0%; Score 393; DB 22;
94.4%; Pred. No. 1.1e-32;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grewal I, Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71914 standard; Protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0182938.
2000US-0226986.
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Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-2000; 2000WO-US32378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashkenazi AJ, Dodge KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-541628/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 GQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD15901
                                                                                                                                                                                                                                             WO200160397-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rACI protein.
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonists
                                                                                                                                                                                                                                                                                                                  23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (an M;
       염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present Sequence Teppersons a numer transmender activator and compared to the present Sequence Teppersons of BR43x2 (an isoform of TACI). Teceptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI coreptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI domain, and are used for inhibiting atthick activity. Zurif is a TNF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA creeptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The associated with an autoimmune disease selected intubody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The Zurif activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, ceptor-ligand engagement is associated with asthma, bronchitis, ceptor-ligand engagement glalure, glomerulonephritis, ransl neoplasms, multiple myelomas, lymphomas, limpuncouppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus. Crohn's disease, joint pain, swelling, anaemia, or septic shock, BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC----CRKEQGKFYDHLLRDCISCASIC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human transmembrane activator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 393; DB 21;
Pred, No. 1.1e-32;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 149-150; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yee DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE09240 standard; Protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gross JA, Xu W, Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 97.0%;
Best Local Similarity 94.4%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                          07-JAN-2000; 2000WO-US00396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholesterol or renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-452538/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 GQHPKQCAYFC 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA58558.
                                                                                                                                     WO200040716-A2.
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Sequence

AAE09240;

XEXEXEX

AAE09240

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us-09-854-864-16.rag

Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autofimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysemi; pyelonephritis; renal neoplasm; multiple mylomoephritis; vascullitis; nephritis; renal neoplasm; multiple myloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; naemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; reppl emboli.

A murine ztnf4, a tumour necrosis factor ligand.

(first entry)

20-0CT-2000

AAY94006;

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The present sequence is a human tumour necrosis factor receptor (TACI) protein. TACI (Transmembrane activator and calcium-signal modulating cyclophilin ligand (CAMI-) interactor) forms a complex with neutrokine alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L complex is useful for modulating an intracellular signalling cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L for therapeutic purposes to intact the interaction between TACI and TACI-L for therapeutic purposes to treat tumour and tumour metastasis and to combat various autoimmune diseases e.g. multiple sclerosis and diabetes, as well as other disorders, such as viral infection, rheumatoid arthritis, graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions and inflammation. The interaction is used to study cellular processes as sociated with tumour necrosis factor (TNF)-receptors such as immune regulation, cell proliferation, cell death and inflammatory responses. The interaction between the extracellular region of TACI and TACI-L can and the complex and the 
neutrokine alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy; neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour; antiartritic; antirheumatic; immunosuppressive; multiple sclerosis; rheumatoid arthritis; graft rejection; inflammation; cell proliferation; cell death; immunoglobulin E-mediated allergic reaction; IgE.
                                                                                                                                                                                                                                                                                /label= Extracellular_domain
/note= "Binds with amino acids 123-285 of extracellular
domain of TACI-L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of new interactions between tumour necrosis factor receptors (TACI) TACI ligands to screen candidate molecules for determining agonist antagonist interactions which are used for treating inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 293;
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Pred. No. 1.1e-32;
0; Mismatches 0;
                                                                                                                                                                                                                            Location/Qualifiers
2..166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Fig 1b; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0302863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodwin RG, Din WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-016005/02
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                                                                                                                                                                                                                                                                                                                                                                                               WO200067034-A1
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000
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                                                                                                                                                                                                                                                         Domain
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Matches
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Yee DP;

Xu W, Madden K,

Gross JA,

WPI; 2000-452538/39.

N-PSDB; AAA58566

(ZYMO) ZYMOGENETICS INC

07-JAN-2000; 2000WO-US00396

WO200040716-A2.

13-JUL-2000

Mus musculus.

99US-0226533

07-JAN-1999;

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The present sequence represents murine ztnf4, a tumour necrosis factor ligand. The extracellular domains of BR432 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or BCMA (a related B cell protein) contain a cysteine rich domain, and are used for inhibiting BR432, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector f-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatold arthritis. The ztnf4 activity and BR332, TACI or BCMA receptor-ligand engagement is associated with a autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatold arthritis. The ztnf4 activity and BR332, TACI or BCMA receptor-ligand engagement is associated with a sthma. bronchitis, emphysema, end stage renal failure, glomerulonephritis, vascullitis, nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft cribic specific shock. BR4322, TACI, and BCMA polypeptides, fusions, antibodies, ceptic shock. BR4322, TACI, and BCMA polypeptides, fusions, antibodies, septic shock. BR4322, TACI, and BCMA polypeptides, fusions, antibodies, septic shock. BR4322, TACI, and became to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%; Score 256; DB 21;
57.7%; Pred. No. 1e-18;
tive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 163; 175pp; English.
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Best Local Similarity
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AAY94006 standard; Protein; 249 AA.

AAY94006 ID AAY94 XX

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RESULT

gqhpkqcayfc 104

GQHPKQCAYFC .67

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joint

be used

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Gaps

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Indels

Length 247;

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nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas
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                light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be us to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases in particularly critical limb ischemia and coronary disease involving abnormal anglogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to 26 secreted human proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection.
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                                                                                                                                                                                                                DB 21;
2.1e-13;
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                                                                                                                                                                                                       50.4%; Scott No. 2.100.0%; Pred. No. 2.100.0%; Pred. No. 2.100.0%; Mismatches
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                                                                                                                                                                                                                                                                                      34 CRKEQGKFYDHLLRDCISCASICGQHPKQCAYFC
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                                                                                                                                                                                                                                                                                                                                                                                                            AAB65001 standard; protein; 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duan RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0137725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein #9
                                                                                                                                                                                                                Query Match 50.4
Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061741/07.
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                                                                                                                                                              247 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200075375-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB65001;
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                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                            AAB65001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.888888888888
                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                            Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoformmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; rend incoplasm; multiple myelomephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft vasus host disease; inflammation; swelling; anemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human BR43x2 polypeptide, which is an isoform of the transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF) receptor. The extracellular domains of BR43x2 factor DEMA (a related B cell protein) contain a cysteine rich domain, and are used for inhibiting zuhf activity. Zinf4 is a TNF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The zinf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25..58
/note= "cysteine-rich pseudo repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting ztnf4 activity in a mammal, to treat
                                                                                                                                                                                                                               Human BR43x2, an isoform of the TACI receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "extracellular domain"
25..58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "transmembrane domain"
134..247
/note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 62; Page 145; 175pp; English.
                                                                                                                       AAY93998 standard; Protein; 247 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yee
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                                                                                                                                                                                              20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121..133
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                    |||:|||:||
66 tqhpqqcahfc 76
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57 GQHPKQCAYFC 67
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                                                                                                                                                           AAY93998;
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Shi Y; Young PE;

Length 220;

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AAY97572;
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                                                    74 cpetmveiwncmnsslpgvfkksdgwvglgccelaialecrgackgasskndiskvcrke 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish
                                1 CPEE--QYWDPL------LGTC----MSCKTICNHQSQRTCAAFCCRKE 37
                                                                                                                                                                                                                     vascular endothelial growth factor; VEGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated vascular endothelial growth factor-D - used to develop products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders
               35;
                                                                                                                                                                                                                                                                                                                                                  /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                       /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                               intestinal malabsorptive syndrome; biopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                   Homo sapiens vascular endothelial growth factor D (VEGF-D).
             27; Indels
                                                                                                                                                                                                                                                                                                                                                                    potential N-linked glycosylation
                                                                                   38 QGKFYDHLLRDCIS-----CASICGQHPKQCAYFC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stacker SA, Wilks AF;
     Pred. No. 0.33;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Pages 57-58; 101pp; English.
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                         AAW53240 standard; Protein; 325 AA
             10;
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96US-0023751.
96AU-0003554.
96US-0031097.
     25.8%;
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                                                                                                                                                                                (first entry)
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258..260
             25; Conservative
                                                                                                                                                                                                                                                                                                                                                          ..158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-179057/16.
Best Local Similarity Matches 25; Conserv
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23-AUG-1996
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                                                                                                                                                            AAW53240;
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                                                                                                                     RESULT 11
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collateral circulation in tissue infarction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood is stream or to improve blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary disease; angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis; rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy; infectious disease; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb ischaemia or coronary disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 cpidmlwdsnkckcvlqeenplagtedhshlqepalcgphmmfdedrcecv-cktpcpkd 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- CMSCKTICNH- 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength 325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76.5;
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9
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24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AA;
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and the DNA sequences encoding them a invention. The anglogemic procession of the DNA sequences encoding them a invention. The anglogemic procession and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of anglogemic protein electring mutations or the presence or amount of anglogemic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit anglogemesis in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rhemmatoid arthritis or psoriasis. Agonists are also used to identify specific increased vascular proteins are also used to identify specific binding agents (potential therapeutic gants) and to raise antibodies. The proteins are also used to identify specific binding agents (potential therapeutic gants) and to raise antibodies. The antibodies are useful as therapeutic (antibognists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapey (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoletic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide range of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating
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  is an anglogenic protein of the invention. The anglogenic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zveqf2 growth factor; mitogen; fibroblast; smooth muscle cell; venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect; angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 cpidmlwdsnkckcvlqeenplagtedhshlqepalcgphmmfdedrcecv-cktpcpkd 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 --QSQRTCAAF-----CCRKEQGKFYDHLL--RDCISCASICGQHPKQCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Cysteine-rich domain""
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24.8%; Pred. No. ...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cysteine-rich domain"
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?95..354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Balbiani ring motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       regeneration of the nervous system etc.
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24..108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW49036;
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The present sequence represents a human zvegf2 growth factor encoded by the zvegf2 cDNA which was isolated from a human heart CDNA library zvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or smooth muscle cells. zvegf2 is claimed to be useful for stimulating the revascularisation of tissue or the re-endothelialisation of vascular tissue. zvefg2 is particularly claimed to be useful for the treatment of full-thickness skin wounds, including venous stasis ulcers and diabetic ulcers. The zvegf2 protein is also claimed to be useful as an additive in tissue adhesives for promoting revascularisation of the healing tissue. Antagonists against zvegf2 can be used to block its mitogenic, chemotactic and anglogenic effects. The antagonists may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitogenic, chemotactic and angiogenic effects. The antagonists may therefore be useful for reducing growth of solid tumours by inhibiting neovascularisation of the developing tumour or by directly blocking tumour cell growth, in the treatment of diabetic retinopathy, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 cpidmlwdsnkckcvlqeenplagtedhshlqepalcgphmmfdedrcecv-cktpcpkd 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CMSCKTICNH- 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascular endothelial growth factor; VEGF-D; anglogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                      New isolated vascular endothelial growth factor - used to develo products for treating e.g. wounds, burns, myocardial infarction, tumours, psoriasis, arthritis, restenosis or organ transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 lighpkncscfeckesletccgk-----hklfhpdtcscedrcpfhtrpca 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 -- QSQRTCAAF------CCRKEQGKFYDHLL--RDCISCASICGQHPKQCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 354;
                                                                                                                                                                                                                           Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens vascular endothelial growth factor D (VEGF-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.9%; Score 76.5; DB 19; 24.8%; Pred. No. 3.4; ive 6; Mismatches 22;
                                                                                                                                                                                                                           Nygaard S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPEEOYWD----------------
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Pages 53-54; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW53241 standard; Protein; 354 AA.
                                                                                                                                                                                                                         Hart CE,
                                                                              97WO-US20888
                                                                                                                    970S-0933455
960S-0759657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis, and scleroderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Conservative
                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                         Gilbert T,
                                                                                                                                                                                                                                                             WPI; 1998-333256/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                    N-PSDB; AAV32823
WO9824811-A2.
                                                                              20-NOV-1997;
                                                                                                                                         06-DEC-1996;
                                                                                                                      8-SEP-1997;
                                                                                                                                                                                                                       Conklin DC,
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Search completed: June 25, 2002, 16:16:10
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                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood in the lung and/or gaseous exchange between the lungs and the blood cremability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, cor to treat malabsorptive syndromes in the intestinal tract.

Ountitation of VEGF-D in cancer blopsy specimens may be useful as an indicator of future metastatic risk. Antegonists can be used involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 cpidmlwdsnkckcvlqeenplagtedhshlqepalcgphmmfdedrcecv-cktpcpkd 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                        New isolated vascular endothelial growth factor-D - used to develop products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76.5; DB 19;
Pred. No. 3.4;
6; Mismatches 22;
                                                                                                                                                                                                                                                          Stacker SA, Wilks AF;
                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Pages 60-61; 101pp; English.
                                                                                                                                                                                                                                  UNIV HELSINKI LICENSING LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW44293 standard; Protein; 354 AA
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                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES (UYHE-) UNIV HELSINKI LICENSIN
                                                                                                               96AU-0001825.
96US-0023751.
96AU-0003554.
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24.8%;
                                                                                                                                                    96US-0031097
97AU-0004954
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Best Local Similarity 24.8
Matches 28; Conservative
                                                                                                                                                                                                                                                          Achen MG, Alitalo K,
                                                                                                                                                                                                                                                                                  WPI; 1998-179057/16.
N-PSDB; AAV20807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 AA;
Homo sapiens.
                         W09807832-A1
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                                                                           21-AUG-1997;
                                                                                                                                                                                            19-JUN-1997
                                                  26-FEB-1998
                                                                                                                                           11-NOV-1996
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05-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CMSCKTICNH- 23
                                                   Human; vascular endothelial growth factor D; VEGF-D; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 -- QSQRTCAAF-----CCRKEQGKFYDHLL--RDCISCASICGQHPKQCA 64
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                                                                                                                                                                                                                                                                                                                                                                                                                  (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Human vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CPEEQYWD-------PLLGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 18-20; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                     97WO-JP02456.
                                                                                                                                                                                                                                                                                                                                                           96JP-0185216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.9°
Best Local Similarity 24.8
Matches 28; Conservative
                                                                                inflammation; oedema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-110591/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirata Y, Nezu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV15156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating oedema
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-290-333-6
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US-08-915-795-3
US-08-915-795-5
US-08-944-941-2
US-08-447-642-2
US-09-236-503-2
PCT-US39-0214-7
US-08-465-380-6
US-08-465-380-6
US-08-486-397-6
US-08-486-397-6
US-08-486-397-41
US-08-481-965-6
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Listing first 45 summaries
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Sequence 41, Appl Sequence 6, Appli Sequence 41, Appl Sequence 6, Appli Sequence 6, Appli Sequence 41, Appl Sequence 41, Appl Sequence 8, Appli	THAT BINDS THE SAME AND METH	Length 166;
28 69.5 17.2 75 3 US-09-249-472-41 29 69.5 17.2 75 3 US-09-249-411-6 30 69.5 17.2 75 3 US-09-249-451-41 31 69.5 17.2 75 3 US-08-249-451-41 32 69.5 17.2 75 3 US-08-809-455-6 33 69.5 17.2 75 3 US-08-809-455-6 34 69.5 17.2 75 3 US-08-461-6 35 69.5 17.2 75 3 US-09-249-461-41 36 69.5 17.2 75 3 US-09-249-461-41 37 69.5 17.2 75 3 US-09-249-48-6 38 69.5 17.2 75 3 US-08-465-39-8 40 69.5 17.2 79 2 US-08-466-39-8 41 69.5 17.2 79 2 US-08-486-39-8 42 69.5 17.2 79 2 US-08-486-39-8 43 69.5 17.2 79 2 US-08-486-39-8 44 69.5 17.2 79 2 US-08-486-39-8 45 69.5 17.2 79 2 US-08-461-86-39-8 46 69.5 17.2 79 2 US-08-461-86-39-8 47 69.5 17.2 79 2 US-08-461-8 48 69.5 17.2 79 3 US-08-461-8 49 69.5 17.2 79 3 US-08-34-641-8	A-6 A-6 A-6 A-6 A-6 A-6 Bram, Richard J I: Bram, Richard J I: Von Bullow, Gotz I: Vo	Query Match 97.0%; Score 393; DB 2; Le

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Sequence 2, Application US/09290333
Patent No. 5316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                                                                             Sequence 2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Von Bullow, Gotz
TITLE OF INVENTION: AL YMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 393; DB 2; Length 29 94.4%; Pred. No. 1.4e-34; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.4
Matches 67; Conservative
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                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          USA
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U ZIP: 07601
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                                                               US-08-810-572A-2
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                                                                                                                                                                                                                                                                                                                                                                       AFFILLANT. DIEST, GOLZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                          Ξ;
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                          Gaps
                                                             1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC----CRKEQGKFYDHLLRDCISCASIC 56
                                                                                        1 CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFC----CRKEQGKFYDHLLRDCISCASIC 56
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 166;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <UNKNOWN>
1 Similarity 94.4%; Pred. No. 8e-35; 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFRAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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94 GQHPKQCAYFC 104
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                            US-09-290-333-6
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193 CPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV-CKTPCPKD 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CPEEQYWD-------PLLGT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76.5; DB
Pred. No. 0.51;
6; Mismatches
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NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
                                                                                                                                                                                                                                              1064/42983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MATC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
ATUTLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
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APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: EVANS. JOSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064,
TELECOMMUICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08915795
Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.9%;
Best Local Similarity 24.8%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                   325 amino acids
                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                   MEDLUM INFORMATION
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: CUNKnown>
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 1340-1-007 PCT
TELEPHONE: 201-487-5300
TELEPHONE: 201-487-5300
TELEPHONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
97.0%; Score 393; DB 4; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.4e-34;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NM, Sulte 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08915795; Patent No. 6235713; GENERAL INFORMATION: APPLICANT: Marc G. ACHEN APPLICANT: Andrew F. WILKS APPLICANT: Steven A. STACKER; APPLICANT: Kari ALITALO ... TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 293 amino acids
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                         ZIP: 07601
COMPUTER READABLE FORM:
                  NUMBER OF SEQUENCES: 11
                                                                                                                                                    STATE: New Jersey
                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                           USA
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                                                                                                                                                                         COUNTRY:
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US-08-915-795-3
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amino acid
                     Best Local Similarity
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US-08-447-642-2
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US-09-236-503-2
  Query Match
                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 CPIDMLWDSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECV-CKTPCPKD 280
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            ----CMSCKTICNH- 23
                                                                                                                                                                                                                                                                                                                                                                                                    Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 LIQHPKNCSCFECKESLETCCQK-----HKLFHPDTCSCEDRCPFHTRPCA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 -- QSQRTCAAF-----CCRKEQGKFYDHLL--RDCISCASICGQHPKQCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
WUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FYVE PALO ALTO SQUARE CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
CLASSIFICATION: 4355
COMPATION: A355
COMPATION: A355
                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                         Score 76.5; DB
Pred. No. 0.55;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISSTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/01US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 843-5070
TELEFAX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PTTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08284941 Patent No. 5863756 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                        iovology: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

TISSUE TYPE: Human Lung
US-08-915-795-5
                   TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                        TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.8%;
Matches 28; Conservative
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 969 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-284-941-2
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CPEEQYWD----
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APPLICANT: Barr, Philip J
APPLICANT: Kiefer, Michael C
APPLICANT: Kiefer, Michael C
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Polypeptides in Cells
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 CMSCKT-ICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISC---ASICGQHPKQC 63
                                                                                                                                                                                                                                                                       Sequence 2, Application US/08447642
Patent No. 599890
GENERAL INFORMATION:
APPLICANT: BARK, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO ALTO SQUARE
18.4%; Score 74.5; DB 2; Length 969; 27.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 74.5; DB 2;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR PAPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 08/284,941
FILING DATE: 2 August 1994
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RTCHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/01US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 843-5070
TELEFRAX: (415) 857-0663
                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 843-5070
TELERAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SED ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.4%;
Best Local Similarity 27.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        969 amino acids
                                               15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA COUNTRY: USA
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3;

Gaps

7;

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212 BAQKWGPECNHLCTACMNNGVCHEDTGECICPPGFWGRTCEKACELHTFGRTCKERCSGQ 271
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                                                                                                     14 CMSCKT-ICNHQSQRTCAAFCCRKEQGKFYDHLLRDCISC---ASIC¢QHPKQC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1124;
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                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,474 FILING DATE: CLASSIFICATION 435 PRIOR APPLICATION WINDER: US 07/905,600 FILING DATE: 26-JUN-1992 ATTORNEY/AGENT INPORMATION: NAME: NAME: CASSIFICATION NUMBER: US 07/905,600 FILING DATE: 26-JUN-1992 ATTORNEY/AGENT INPORMATION:
                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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4; Mismatches
         Pred. No. 2.3;
9; Mismatches
                                                                                                                                                                                                                          Sequence 2, Application US/08323474
Patent No. 5447860
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US93-06093-2
Sequence 2, Application PC/TUS9306093
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 EGCKSYVFCLPDPYGCSCATGWKGLQCNEAC 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 587-0430
TELEFAN: (206) 233-0644
TELEFAN: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.38;
26.48;
         27.8%;
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                             Conservative
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Best Local Similarity 26.4
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-323-474-2
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
         Best Local Similarity
                                                                                                                                                                                     RESULT 11
US-08-323-474-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9302147A
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: RIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GOOWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 74.5; DB 4; Length 969;
Pred. No. 2.3;
9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIFICATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH D., RICHARD L
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: 30092
TELECOMMUNICATION INFORMATION:
                      CURRENT APPLICATION NUMBER: US/09/236,503
CURRENT FILING DATE: 1999-01-25
EARLIER APPLICATION NUMBER: 08/447,642
EARLIER FILING DATE: 1995-05-23
EARLIER FILING DATE: 1995-05-23
EARLIER FILING DATE: 1994-08-02
EARLIER FILING DATE: 1994-08-02
EARLIER FILING DATE: 1992-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                    18.4%;
27.8%;
FILE RÉFERENCE: CHIR-009/04US
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 27.8 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein PCT-US93-02147A-2
                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-503-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
PCT-US93-02147A-2
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                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 969
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ò q 3;

26;

DB 5;

18.4%; Score 74.5;

Query Match

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OFFWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFFTANTON.
                                                                                                                                                                                                                                                   213/268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-465-380-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SCKTICN-HQSQRTCAAFCCRK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-465-380-6
Sequence 6, Application US/08465380
Patent No. S863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yoes R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
UNMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 5;
Pred. No. 8;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 35° Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 EGCKSYVFCLPDPYGCSCATGWKGLQCNEAC 302
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06093
FILING DATE: 19930625
CLASSIFICATION: PCT/US93/06093
FILING DATE: 19930625
CLASSIFICATION NUMBER: 05 07/905,600
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 2609
TELECHONER: 2605
TELECHONER: (206) 58-0430
TELECHONE: (206) 58-0430
TELECHONE: (206) 58-0430
TELERAX: 756822
INFORMATION: OF SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 11124 Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 EQGKFYDHLLRDCISCASICGQHPKQCAYFC 67
                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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Best Local Similarity 26.4%;
Matches 24; Conservative
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                                               Seattle
Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                              SOFTWARE:
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                                                                                    COUNTRY:
                                                                  STATE:
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4 PECGENEWLDVCGTKKPCEAKCSEEEEEDPICRSFSCPGPAACVCEDGFYRDTVIGDCVK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
17.2%; Score 69.5; DB 2; Length 75;
Best Local Similarity 27.9%; Pred. No. 0.69;
Matches 19; Conservative 10; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/08465380

Sequence 41, Application US/08465380

Batent No. 5863894

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Journal H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yearnick G.J. Gansemans, Matthew Moyle, APPLICANT: Yearnick G.J. Gansemans, Matthew Moyle, APPLICANT: Pannick G.J. Gansemans, Matthew Moyle, APPLICANT: PROTEIN

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT; TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: Salle 4700

CITY: Los Angeles

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: June 5, 1995
PRICR APPLICATION DATA:
APPLICATION TO THE STATE OF THING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEX/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 31,158
REGISTRATION NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 anino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
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Search completed: June 25, 2002, 16:12:13 Job time: 53 sec
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Best Local Similarity 27.98
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 17.2%; Score 69.5; DB 2; Length 75; Best Local Similarity 27.9%; Pred. No. 0.69; Matches 19; Conservative 10; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YANNICK GEORGES JOJET APPLICANT: GANSERAND APPLICANT: GANSERAND THE OF INVENTION: COAGULANT PROTEIN NUMBER OF SEQUENCES: 86 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEORGE P. VLASUK; PATRICK ERIC
HUGO STANSENS; JORIS HILDA
LIEVEN MESSENS; MARC JOZEF
LAUWEREYS; YVES REHE LAROCHE;
LAUMERNY STEPHANE JESPERS; and
YANNICK GEORGES JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASSESO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
AFFLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTOREX/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-160
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: CASSO ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acids
TYPE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                    Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application US/08480478 Patent No. 5864009 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
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APPLICANT:
APPLICANT:
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APPLICANT:
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28; Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PE--EQYWDPLLGTCMSCKTICNHQSQR--TCAAFCCRK-----EQGKFYDHLLRDCIS 51
                                                                                                                                                                                                                                                                                                                                      Length 75;
                                                                                                                                                                                                                                                                                                                                    17.2%; Score 69.5; DB 2;
27.9%; Pred. No. 0.69;
tive 10; Mismatches 28;
| REFERENCE/DOCKET NUMBER: 208/290 | TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 469-1600 | TELEFAX: (213) 955-0440 | TELEFEX: 67-3510 | TELEFX: 67-3510 | SEQUENCE CHARACTERISTICS: LENGTH: 75 amino acids | TYPE: amino acid TOPOLOGY: linear US-08-480-478-35
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Wed Jun 26 06:00:10 2002